

Supporting Information for

Glial dysregulation in human brain in Fragile X-associated tremor/ataxia

syndrome

Caroline M. Dias, Biju Issac, Liang Sun, Abigail Lukowicz, Maya Talukdar,

Shyam K. Akula, Michael B. Miller, Katherine Walsh, Shira Rockowitz,

Christopher A. Walsh

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Other supporting materials for this manuscript include the following excel files:

Datasets S1-S20



Figure S1: **Experimental and bioinformatic filtering pipeline and quality control metrics. A.** Representative gating strategy to obtain initial nuclei for encapsulation and subsequent bioinformatic processing. **B.** Overall group comparisons of number of genes/nuclei (features), counts/nuclei (UMI) and % mitochondrial gene expression in CON, FXPM, and FXS cases from left to right by region. **C.** UMAP depicting cell-type specific and condition specific differences in metrics in frontal cortex. Top row is number UMI, middle is number of genes, and bottom is mitochondrial gene percentage. (CON, FXPM, FXS from left to right). Clusters are described in Figure 1D.



Figure S2: **Demographic and sample information. A.** No significant differences between groups with respect to age and PMI. FXS samples had lower RIN than control but not premutation cases (p<.05, one-way ANOVA, post-hoc Tukey's test). **B.** No significant correlation between RIN & Age, PMI & Age, or RIN & PMI among samples. **C**. Western blotting of frontal cortex premutation and FXS samples demonstrating variably reduced FMRP in premutation cases and absent FMRP in FXS cases. From left to right: 4664 (PM), 4806 (FXS), 5408 (CON), 5006 (PM), 5319 (FXS), 5657 (CON), 4555 (PM), 5497 (CON), 1793 (CON). Blots cropped for clarity.



Figure S3: **High resolution frontal cortex cell-type specific markers are concordant with broader classification.** Note layer specific (CUX2, RORB, TLE4, SEMA3A, NTNG2) and inhibitory neuron subcluster specific (SST, VIP, PVALB, SV2C) expression.



Figure S4: **Frontal cortex oligodendrocyte lineage markers.** Violin plots demonstrating distinct gene expression patterns in oligodendrocyte lineage clusters revealing a spectrum of developmental states.



Figure S5: Pseudobulk analysis of frontal cortex neuronal subpopulations. This analysis reveals no significant changes in FMR1 mRNA in neurons in PM cases. Note significant downregulation in FXS cases despite the smaller n. Orange *: reduced FMR1 in FXS vs CON padj< .05.







Figure S6: **FMR1 mRNA expression. A.** RNAscope demonstrates no change in FMR1 expression in all cells (left) or nuclei (right). (two-tailed t-test, p>.05) **B.** Distribution of FMR1 expression in all nuclei, binned by # of dots/nuclei, and separated by sample.

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Figure S7: **Heterogeneity in FMR1 expression by donor. A.** snRNA-seq FMR1 expression in cerebellum separated by individual. **B.** There is a significant association between FMR1 expression in cortical microglia and premutation repeat size. **C.** Frontal cortex snRNA-seq FMR1 expression separated by individual. FMR1 heatmap shows average expression.



Figure S8: Lack of glial cluster alterations in premutation BA22. BA22 of 5746 demonstrates glial percentage comparable to control BA10, rather than premutation BA10 (see Table 2). Default clustering and tSNE plot output from Cell Ranger displayed, cell clusters for mature oligodendrocyte and astrocytes identified with PLP1 and AQP4 markers.



Figure S9: Association between cortical inhibitory neuronal density (inhibitory/total neuron percentage) and age regardless of Fragile X status. Blue: control, grey: FXS, orange: FXPM.



% Unique DEG in Age	PM vs CON	FXS vs CON	PM vs FXS
Granule	0	0	0
Bergmann Glia	0	0.2%	0.1%
Interneuron II	0	4.3%	4.1%

% Unique DEG in PMI	PM vs CON	FXS vs CON	PM vs FXS
Granule	0	0	0
Bergmann Glia	0.4%	0.8%	0.3%
Interneuron II	0	1.7%	5.9%

% Overlap in No Variable	PM vs CON	FXS vs CON	PM vs FXS
and Age Lists			
Granule	100%	100%	98.9%
Bergmann Glia	98.7%	61.9%	90.2%
Interneuron II	99.7	32.1	81.1%

% Overlap in No Variable	PM vs CON	FXS vs CON	PM vs FXS
and PMI Lists			
Granule	96.9%	91.4%	98.9%
Bergmann Glia	62.1%	93.1%	63.5%
Interneuron II	80.1	72.1	55%

Figure S10: Analysis of effects of age and PMI on gene expression. PCA plots demonstrating variability grouped by age (above and below 50 years old) and PMI (above and below 12 hours post-mortem). MAST was used to generate cell-type-specific differential expression lists with age and PMI independently and compared to gene lists without these variables. Inclusion of these variables did not add significant additional information (i.e. new unique DEG). The overlap of the no variable analysis and including age analysis, and no variable and PMI analysis, were largely concordant, except for some FXS comparisons. There was no change in significance of FMR1 (or lack thereof) within any of these gene lists although the precise padj varied.



Figure S11. Pseudotime reclustering. **A.** Reclustering demonstrates breakdown of conditions. **B.** Demonstration of two oligodendrocyte branches identified by reclustering. **C.** Markers of oligodendrocyte maturity and FMR1. **D.** Density plot of cell type distribution in branch 1 (left) and branch 2 (right).



Figure S12 Differential expression in pseudotime. **A.** FXS vs. control comparisons in cortex pseudotime trajectory for branch 1. Heatmap shows top differentially expressed genes (pairwise comparison, Wald statistic). **B.** FXS vs. control comparisons in cortex pseudotime trajectory for branch 2. **C.** Cerebellar pseudotime reclustering broken down by condition (top right) and cell type (bottom right). **D.** Premutation vs. control comparisons in cerebellar pseudotime trajectory. Heatmap shows top differentially expressed genes.

		-18	8_
Astro I	1411	768	643
Astro II	1690	792	898
Endo	712	351	361
Inh-PVALB I	296	244	52
Inh-PVALB II	13	11	2
Inh-SST	368	245	123
Inh-SV2C I	494	350	144
Inh-SV2C II	2	1	1
Inh-VIP	332	261	71
L2 3-4	165	100	65
L5 6 I	6	5	1
L5 6 II	0	0	0
Microglia	1443	699	744
MOL	590	395	195
Neu L4 I	239	209	30
Neu L4 II	165	135	30
Neu NRGN	1464	915	549
Neu NTNG2	0	0	0
OLI	1565	924	641
OL II	1936	931	1005
OPC	1907	894	1013

Cell_Type \U00e9 DEG_Count \U00e9 Upreg_Count \U00e9 Downreg_Count \U00e9

Table S1: Number of differentially expressed genes in frontal cortex clusters FXS vs

control. Abbreviations as in Figure 1

Cell_Type 🗄	DEG_Count 🗄	Upreg_Count 🗄	Downreg_Count ‡
Astro I	385	223	162
Astro II	691	371	320
Endo	20	20	0
Inh-PVALB I	280	144	136
Inh-PVALB II	173	64	109
Inh-SST	248	118	130
Inh-SV2C I	138	59	79
Inh-SV2C II	116	55	61
Inh-VIP	193	74	119
L2 3-4	293	151	142
L5 6 I	74	43	31
L5 6 II	38	27	11
Microglia	673	357	316
MOL	421	179	242
Neu L4 I	143	79	64
Neu L4 II	142	78	64
Neu NRGN	1540	900	640
Neu NTNG2	278	179	99
OLI	1557	930	627
OL II	16	11	5
OPC	453	241	212

	OPC	455	241	212			
٦	Table S2: I	Number of d	lifferentially e	expressed gen	es in frontal	cortex	clusters

premutation vs control.

Cell_Type ≑	DEG_Count ≑	Upreg_Count 🔅	Downreg_Count 🗧
Astro I	1518	773	745
Astro II	1986	1157	829
Endo	211	123	88
Inh-PVALB I	673	345	328
Inh-PVALB II	74	41	33
Inh-SST	706	351	355
Inh-SV2C I	687	323	364
Inh-SV2C II	8	3	5
Inh-VIP	704	274	430
L2 3-4	518	257	261
L5 6 I	52	21	31
L5 6 II	2	0	2
Microglia	1447	770	677
MOL	1282	517	765
Neu L4 I	447	192	255
Neu L4 II	350	167	183
Neu NRGN	252	107	145
Neu NTNG2	15	4	11
OLI	1987	1197	790
OLII	781	362	419
OPC	1709	940	769

Table S3: Number of differentially expressed genes in frontal cortex clusters
 premutation vs FXS.

Cell_Type 🔶	DEG_Count \\$	Upreg_Count 🔶	Downreg_Count
Astrocyte	867	408	459
Bergmann Glia	1176	667	509
Endothelial	1	1	0
Granule	816	532	284
Interneuron II	216	105	111
Interneuron	149	115	34
Microglia	11	7	4
Oligo	337	221	116
OPC	202	152	50
Purkinje	0	0	0

Table S4: Number of differentially expressed genes in cerebellum clusters FXS vs

 control.

Cell_Type 🔷	DEG_Count 🔷	Upreg_Count 🔷	Downreg_Count
Astrocyte	209	96	113
Bergmann Glia	226	143	83
Endothelial	3	2	1
Granule	161	75	86
Interneuron II	336	128	208
Interneuron	486	165	321
Microglia	125	57	68
Oligo	123	73	50
OPC	38	29	9
Purkinje	1	1	0

 Table S5: Number of differentially expressed genes in cerebellum clusters premutation

 vs control.

Astrocyte	1345	787	558
Bergmann Glia	1267	617	650
Endothelial	1	1	0
Granule	1024	425	599
Interneuron II	540	172	368
Interneuron	500	240	260
Microglia	126	58	68
Oligo	371	119	252
OPC	360	143	217
Purkinje	0	0	0

 $\label{eq:cell_type} \begin{array}{c} & \textbf{DEG_Count} \Leftrightarrow & \textbf{Upreg_Count} \Leftrightarrow & \textbf{Downreg_Count} \Leftrightarrow \end{array}$

Table S6: Number of differentially expressed genes in cerebellum clusters premutationvs FXS.

		Differential expression along the trajectory	Differential expression between conditions
	Comparison	Genes selected (q-value < 0.05, Moran's I > 0.1)	Genes with the p.adj < 0.05
	FXPM vs CON		383
Branch 1	FXS vs CON	1042	436
	FXPM vs FXS		695
	FXPM vs CON		296
Branch 2	FXS vs CON	1000	741
	FXPM vs FXS		597

 Table S7: Number of differentially expressed genes in pseudotime analysis.

matif	TE bigbConf	TE lowConf	NES
transfac_pro_M02771	IRF9 (inferredBy_Orthology).	IRF5 (inferredBy_MotifSimilarity_n_Orthology).	4.95
		IRF1; IRF2; IRF3; IRF4; IRF5; IRF6; IRF7; IRF8; IRF9	
factorbookSTAT2	STAT1; STAT2 (directAnnotation).	(inferredBy_MotifSimilarity).	4.72
issnar MA05171	STAT2 (direct annotation)	IRF1; IRF2; IRF3; IRF4; IRF5; IRF6; IRF7; IRF8; IRF9; STAT1 (inferredBy, MotifSimilarity)	4 19
Jaspar_Www.517.1	STATE (uneconnotation).	ELET- ETV6- GABPA- IRE2- IRE3- IRE4- IRE5- IRE6- IRE7- IRE8- IRE9-	4.15
		POLR2A; PRDM1; RELA; STAT1; STAT2; TBL1XR1	
		(inferredBy_MotifSimilarity). SPIB	
dbcorrdb_IRF1_ENCSR000EGK_1_m1	IRF1 (directAnnotation).	(inferredBy_MotifSimilarity_n_Orthology).	4
cisbpM4635	STAT2 (directAnnotation).	(inferredBy_MotifSimilarity).	3.94
		IRF1; IRF2; IRF4; IRF5; IRF7; IRF8; IRF9; STAT1; STAT2	
cisbpM5572	IRF3 (directAnnotation).	(inferredBy_MotifSimilarity).	3.93
cisbpM5580	IRF9 (directAnnotation).	IRF2; IRF3; IRF4; IRF5; IRF7; IRF8 (inferredBy_MotifSimilarity).	3.91
taipale IRF3 full NNRRAAAGGAAACCGAAACTN repr	IRF3 (directAnnotation).	IRF1; IRF2; IRF4; IRF5; IRF7; IRF8; IRF9; STAT1; STAT2 (inferredBy MotifSimilarity).	3.87
		EP300; IKZF1; IRF1; IRF2; IRF3; IRF4; IRF5; IRF6; IRF7; IRF8; IRF9;	
		PRDM1; SPI1; STAT2; STAT3; TBL1XR1	
dbcorrdb_STAT1_ENCSR000FAU_1_m1	STAT1 (directAnnotation).	(inferredBy_MotifSimilarity).	3.82
taipale_IRF9_full_AWCGAAACCGAAACY	IRF9 (directAnnotation).	IRF2; IRF3; IRF4; IRF5; IRF7; IRF8 (interredBy_Motifsimilarity).	3.79
		IRF9: MTA3: PRDM1: SPI1: SPI8: STAT1: STAT2: STAT3: TBL1XR1	
hocomoco_IRF1_MOUSE.H11MO.0.A	IRF1 (inferredBy_Orthology).	(inferredBy_MotifSimilarity).	3.67
taipaleIRF4_full_NCGAAACCGAAACYN_repr	IRF4 (directAnnotation).	IRF2; IRF3; IRF5; IRF7; IRF8; IRF9 (inferredBy_MotifSimilarity).	3.66
		IRF1; IRF2; IRF3; IRF4; IRF5; IRF7; IRF9	2.00
taipale_cyt_meth_ikr8_NtG/00G7G/00G7N_FL	IRF8 (directAnnotation).	(InterredBy_Motifsimilarity). IRE1: IRE2: IRE4: IRE5: IRE6: IRE7: IRE8: IRE9: STAT1: STAT2	3.58
cisbpM6309	IRF3 (directAnnotation).	(inferredBy_MotifSimilarity).	3.57
cisbp_M6485		SPI1; SPIB; SPIC (inferredBy_MotifSimilarity).	3.56
cisbpM5579	IRF8 (directAnnotation).	IRF2; IRF3; IRF4; IRF5; IRF7; IRF9 (inferredBy_MotifSimilarity).	3.55
taipale_IRF8_full_NCGAAACCGAAACT	IRF8 (directAnnotation).	IRF2; IRF3; IRF4; IRF5; IRF7; IRF9 (interredBy_MotifSimilarity).	3.52
neph UW.Motif.0391	no 2, milo (un econnotacion).		3.49
		BCL11A; EP300; IKZF1; IRF1; IRF3; IRF4; IRF5; IRF6; IRF7; IRF8;	
		IRF9; MTA3; PRDM1; SPI1; SPIB; STAT1; STAT2; STAT3; TBL1XR1	
hocomoco_IRF2_HUMAN.H11MO.0.A	INF2 (directAnnotation).	(InterredBy_MotifSimilarity).	3.46
		(inferredBy_MotifSimilarity), CERPA: CERPG	
cisbpM6277	HLF (directAnnotation).	(inferredBy_MotifSimilarity_n_Orthology).	3.43
		IRF1; IRF2; IRF3; IRF4; IRF5; IRF6; IRF7; IRF8	
taipale_cyt_methIRF9_NYGAAASYGAAACYN_FL_meth	IRF9 (directAnnotation).	(inferredBy_MotifSimilarity).	3.41
		CEBPA; CEBPD; CEBPE; CEBPG; EP300; HLF; PPARGC1A	
cisbp_M0315	CEBPB (inferredBy_Orthology).	(inferredBy_MotifSimilarity_n_Orthology).	3.41
		IRF2; IRF3; IRF4; IRF5; IRF6; IRF7; IRF8; IRF9; PRDM1; RELA;	5.44
homerGAAAGTGAAAGT_IRF1	IRF1 (directAnnotation).	STAT3; TBL1XR1 (inferredBy_MotifSimilarity).	3.4
cisbp_M1271			3.4
tainale cvt meth SPIB RAWWGMGGAAGTN FI	SPIR (direct Apportation)	BCL11A; ELF1; ELF2; ELF4; EP300; IKZF1; IRF4; IRF8; SPI1; SPIC (inferredBy, MotifSimilarity)	3 38
cisbp M5573	IRF4 (directAnnotation).	IRF2; IRF3; IRF5; IRF7; IRF8; IRF9 (inferredBy MotifSimilarity).	3.38
		ATF2; CEBPB; CEBPD; DBP; NFIL3; TEF	
		(inferredBy_MotifSimilarity). CEBPA; CEBPG	
hocomoco_HLF_HUMAN.H11MO.0.C	HLF (directAnnotation).	(inferredBy_MotifSimilarity_n_Orthology).	3.35
taipale cvt meth IRF5 NYGAAACCGAAACY FL	IRF5 (direct Appotation).	IRF1; IRF2; IRF3; IRF4; IRF7; IRF8; IRF9 (inferredBy_MotifSimilarity).	3.31
apacetonen_nastratecorrectore	no stan eeron otation,	ATF2; CEBPE; DBP; NFIL3; TEF (inferredBy_MotifSimilarity).	5.54
taipaleHIf_DBD_NRTTACGTAAYN	HLF (inferredBy_Orthology).	CEBPA (inferredBy_MotifSimilarity_n_Orthology).	3.3
		BCL11A; EP300; FOXM1; IRF9; MTA3; PRDM1; RELA; SPI1; STAT1;	
transfac_pro_M00772	IRF1; IRF2; IRF3; IRF4; IRF5; IRF6; IRF7; IRF8 (directAnnotation).	STAT2; TBL1XR1 (inferredBy_MotifSimilarity).	3.29
transfac pro_M06762	ZNF222 (directAnnotation).	INFR, IBCIXKI (Interedby_Wottsinnarty).	3.28
		IRF1; IRF3; IRF4; IRF5; IRF7; IRF8; IRF9	
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taipaie_cyt_methIKF2_YGAAASYGAAAS_FL	IKP2 (direct/eniocation).	1 1	5.20
taipaie_cyt_meth_ikt2_tGAAASYGAAAS_FL transfac_proM06268	ZNF260 (directAnnotation).		3.27
taipale_cyt_meth_iRt2_yGAAASYGAAACYN Ei	INF2 (direct/annotation). ZNF260 (direct/annotation).	IRF1; IRF2; IRF3; IRF4; IRF5; IRF7; IRF8	3.27
talpale_cyt_meth_iRF9_NYGAAASYGAAACYN_FL talpale_cyt_meth_iRF9_NYGAAASYGAAACYN_FL	IRF9 (directAnnotation). IRF9 (directAnnotation).	IRF1; IRF2; IRF3; IRF4; IRF5; IRF7; IRF8 (InferredBy_MotifSimilarity). IRF1; IRF2; IRF4: IRF8; IRF9 (InferredBy_MotifSimilarity). PRDM1	3.27
taipaie_cyr_meth_IRF9_NYGAAASYGAAACYN_FL taipaie_cyr_meth_IRF9_NYGAAASYGAAACYN_FL taipaie_IRF7_D8D_NCGAAANYGAAACY_repr	IRF2 (une connection). ZNF260 (directAnnotation). IRF9 (directAnnotation).	IRE1; IRE2; IRE3; IRE4; IRE5; IRE7; IRE8 (inferredby_MottiSimilarity). IRE1; IRE2; IRE4; IRE8; IRE9 (inferredby_MottiSimilarity). PRDM1 (inferredby_MottiSimilarity_n_Orthology).	3.27 3.27 3.26
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Lapaze pro, mem. Jin X, Jouron Junos y L Lapaze pro, mem. Jin X, Jouron Junos y L Lapaze cyt, meth. JIRF3, VIGAAANGGAAACYI, pri Lapaze cyt, meth. JIRF3, VIGAAANGGAAACYI, cypr Lapaze cyt, meth. JIRF3, VIGAAANGGAAACYI, cypr Lapaze cyt, meth. JIRF3, VIGAAANGGAAACYI, cypr Lapaze cyt, meth. JIRF3, VIGAAANGGAAACYI, L, meth Lapaze cyt, meth. JIRF3, VIGAAANGGAAACYI, L, meth Labor meth. JIRF3, LENCSBOOOTGU, J, m1 thaimer, JMOOO238 Labor meth. JIRF3, LENCSBOOOTGU, J, m1 transfic, pro_MO7045 Lapaze cyt, meth. JIRF4, VIGAAANGGAACYI, FL	Mr 4 Source and A set of the set	1 11 1 12 18/5; 18/7; 18/9; 1 12 18/5; 18/7; 18/9; 1 18/7; 18/7; 18/9; 18/7; 18/9; 1 17 18/7; 18/9; 1 18/7; 18/7; 18/9; 18/7; 1 18/7; 18/7; 18/9; 18/7; 1 18/7; 18/7; 18/9; 1 18/7; 18/7; 18/9; 18/7; 1 18/7; 18/7; 18/9; 18/7; 18/9; 1 18/7; 18/7; 18/9; 18/7; 18/9; 18/7; 18/9; 18/7; 18/9; 18/7; 18/9; 18/7; 18/9; 18/7; 18/9; 18/7; 18/9; 18/7; 18/9; 18/7; 18/9; 18/7; 18/9; 18/7; 18/9; 18/7; 18/9; 18/7; 18/9; 18/7; 18/9; 18/7; 18/9; 18/7; 18/7; 18/7; 18/7; 18/7; 18/7; 18/7; 18/7;	127 327 326 326 326 326 325 325 324 322 322 322 322 322 322 322 322 322
Lapaze gr., meth Inf Z _ LOUKON LOUKS J1 Lapaze gr meth Inf Z _ LOUKON LOUKS J1 Lapaze _ gr., meth Inf Z _ NYGAAKYGAAKCYI, F1 Lapaze _ gr., meth Inf Z _ NYGAAKYGAAKCYI, gr. Lapaze _ gr., meth Inf Z _ NYGAAKYGAAKSYN, gr. Lapaze _ gr., meth Inf Z _ NYGAAKYGAAKSYN, gr. Lapaze _ gr., meth Inf Z _ NYGAAKYGAAKSYN, J1, meth Lapaze _ gr., DR0595 Lapaze _ gr., DR0596 Lapaze _ gr., DR0596 Lapaze _ gr., meth Inf Z _ NYGAAKYGAAKSYN, J1 Lapaze _ gr., meth Inf Z _ NYGAAKYGAAKYN, J1 Lapaze _ gr., meth Inf Z _ NYGAAKYGAAKYN, J1 Lapaze _ gr., meth Inf Z _ NYGAAKYGAAKYN, J1 Lapaze _ gr., meth Inf Z _ NYGAKYGAKYN, J1 Lapaze _ gr., meth Inf Z _ NYGAKYGAKYN, J1 Lapaze _ gr., meth Inf	Mr 2 BOURDINGEOD, Mr 2 BOURDINGEOD, MR 7 (directAnotation), MR 7 (di	101 102 103 104 <td>1327 3327 336 336 336 335 335 332 332 332 332 332 332 332 332</td>	1327 3327 336 336 336 335 335 332 332 332 332 332 332 332 332
Lapaze pro, mem. Jin X, Jouron Juno 2; L Lapaze pro, mem. Jin X, Jouron Juno 2; L Lapaze pro, mem. JIRR JINGAAANGAAACYI pri Lapaze pro, mem. JIRR JINGAAANGAAACYI pro Lapaze pro, JINGAAANGAAACGAAACYI Lapaze pro, JINGAAANGAAACGAAACYI pro, JINGAAANGAA Lapaze pro, JINGAAANGAAACGAAACYI pro, JINGAAANGAA Lapaze pro, JINGAAANGAAACGAAACYI pro, JINGAAANGAA Lapaze pro, JINGAAANGAAAANGAAACGAAACYI pro, JINGAAANGAAANGAA Lapaze pro, JINGAAANGAAACGAAACYI pro, JINGAAANGAAANGAA Lapaze pro, JINGAAANGAAACGAAACYI pro, JINGAAANGAAANGAA Lapaze pro, JINGAAANGAAACGAAACYI pro, JINGAAANGAAANGAAANGAA Lapaze pro, JINGAAANGAAANGAAANGAAANGAA Lapaze pro, JINGAAANGAAANGAAANGAAANGAA Lapaze pro, JINGAAANGAAANGAAANGAAANGAA Lapaze pro, JINGAAANGAAANGAAANGAAANGAAANGAAANGAA Lapaze pro, JINGAAANGAAANGAAANGAAANGAAANGAA Lapaze pro, JINGAAANGAAANGAAANGAAANGAAANGAAANGAAANGA	MR 5 GirectAnnotation). MR 6 GirectAnnotation). MR 6 GirectAnnotation). MR 7 GirectAnnotatio	No.1 No.1 No.1 <td>1327 332 336 336 336 333 333 334 332 332 332 332 332 332 332</td>	1327 332 336 336 336 333 333 334 332 332 332 332 332 332 332
Lapaze pro, mem. Jin Z., Jouron Junos Jr. Lapaze pro, London J. J. J. Journal J.	MR 2 BOURD IN LABOR MR 2 BOURD IN LABOR 2010 MR 2 BOURD IN LABOR 2010 MR 2 Bourd In Labor MR 2 Bour MR 2 Bour	1 1	1327 3327 336 336 335 335 335 335 332 332 332 332 332 332
Lapaz pr. met IHF _ TUNCONTONOO JL Lapaz pr. Monton JL _ TUNCONTONOO JL Lapaz c.pt, met IHF _ INGANOGANCYANY FL Lapaz c.pt, met IHF _ INGANOGANCYANY cost Lapaz c.pt, met IHF _ INGANOYGANCYANY cost Lapaz c.pt, met IHF _ INGANOYCANY cost Lapaz c.pt, met IHF _ INGANOYCANY cost Lapaz c.pt, me	Mar Laborational Control (Control (Contro))))))))))))))))	NP11, NP2, 1043, 1044, 1045, 1077, 1048 (InferredBy_MotiSimilarity, DifferredBy_Mot	1327 337 336 336 335 335 335 332 332 332 332 332
Lippid cyt, meth. Jin Z, Jouron Juno J; L Lippid cyt, meth. Jin Z, Jouron Juno J; L Lippid cyt, meth. JiR9 JNGAANYGAACY (pp) Lippid cyt, meth. JR9 JNGAANYGAACY (pp)	MAY 26 (directAnotation). MP39 (directAnotation). MP39 (directAnotation). MP3 (directAnotation). MP31 (MP32, MP32, MP33) (nderredby_Official). MP31, MP32, MP32, MP33, MP34, MAF5, MAF5, MAF5, MAF5, MP31, MP32, MP32, MP33, MP33, MP34, MP33, MP33, MP34, MP33, MP34, MP	1 1	1327 3327 336 336 335 335 335 344 344 344 344 344
Lapaz erg, meth Jin 7,	More parameters M	Internetity Internetity Internetity	1327 3327 336 336 335 335 335 3328 3324 3324 3324 3324 3324 3324 3323 3325 3325 3325 3325 3325 3325 3325 3325 3325 3325 3325 3325 3325 3325 3326 3356
Lapaze pr, mem. Jmr. 2	Mr 2 Sourcemutation). Mr 2 Sourcemutation). Hr 3 Sourcemutation). Hr 4 Sourcemutation).	No.1 No.1 No.1 <td>127 127 127 127 127 128 129 129 129 129 129 129 129 129</td>	127 127 127 127 127 128 129 129 129 129 129 129 129 129
Lapaz erg, meth	MAY 20 (directAnotation). MAY 20 (directAnotation). H879 (directAnotation). H879 (directAnotation). H873 (directAnotation). H873 (directAnotation). H873 (directAnotation). H878 (directAnotation). H874 (directAnota	No.1 No.1 <td< td=""><td>1327 337 336 336 335 335 335 332 332 332 332 332</td></td<>	1327 337 336 336 335 335 335 332 332 332 332 332
Lapaze pr, meth. Jin Z., Touron Hundon, 214 Lapaze pr, meth. Jin Z., Touron Hundon, 214 Lapaze pr, meth. JIRF3, VIGAAANGGAAACY (PPT Lapaze pr, meth. JIRF3, VIGAAANGGAAACY (PPT) Lapaze pr, JIRF3, JIRF3, VIGAAANGGAAACY (PPT) Lapaze pr, JIRF3, JIRF3, VIGAAANGGAAACY (PPT) Lapaze pr, JIRF3, JIRF3, JIRF3, VIGAAANGGAAACY (PPT) Lapaze pr, JIRF3, JIRF3, JIRF3, VIGAAANGGAAACY (PPT) Lapaze pr, JIRF3,	Mr 4 Source and A set of the set	1 1	1327 332 336 336 336 335 344 335 344 344 344 344 344
Lapaze pro, mem. Jin Z., Jouron Junos Jr. Lapaze pro, Monos Jin Z., Jouron Junos Jr. Lapaze pro, Lineth. JIRS J. NIGAAANGAAACY repr Lapaze pro, mem. JIRS J. NIGAAANGAAACY repr Lapaze pro, mem. JIRS J. NIGAAANGAAACY repr Lapaze pro, mem. JIRS J. NIGAAANGAAASON _0.08D Lapaze pro, mem. JIRS J. NIGAAANGAAASON _0.08D Lapaze pro, mem. JIRS J. NIGAAANGAAASON _0.08D Lapaze pro, JIRS J. NIGAAANGAAASON _0.08D Lapaze pro, JIRS J. NIGAAANGAAASON _0.000 Lapaze pro, JIRS J. NIGAAAGGAAASON _0.0000 Lapaze pro, JIRS J. NIGAAAGGAAASON _0.00000 Lapaze pro, JIRS J. NIGAAAGGAAASON _0.00000 Lapaze pro, JIRS J. NIGAAAGGAAASON _0.000000 Lapaze pro, JIRS J. NIGAAAGGAAASON _0.00000000 Lapaze pro, JIRS J. NIGAAAGGAAASON _0.0000000000 Lapaze pro, JIRS	Mr 2 go Augustania (a) Mr 2 go (InterAnnotation). MR7 (directAnnotation). MR7 (directAnnotati	1 1	1327 337 336 336 335 335 335 334 334 334 332 332 332 332 332
Lippi2.grv, methBF2_INGAAASYGAAASYL_Lippi2.grv, methBF3_INGAAASYGAAASYL_F1 Lippi2.grv, methBF3_INGAAASYGAAASYL_GAB Lippi2.grv, methBF3_INGGAAASYGAAASYL_GBD Lippi2.grv, methBF3_INGGAAASYGAAASYL_GBD Lippi2.grv, methBF3_INGGAAASYGAAASYL_GTvP Lippi2.grv, methBF3_INGGAASYGAAASYL_GTVP Lippi2.grv, methBF3_INGGAASYGAASSYL_GTVP Lippi2.grv, methBF4_INGGAASYGAASSYL_GTVP Lippi2.grv, methBF4_INGGAASYGGAASSYL_GTVP Lippi2.grv, methB	MR 4 Source and a set of the set	RP11; RP2; RP3; RP3; RP3; RP3; RP3 RP11; RP2; RP3; RP4; RP3; RP3; RP3; RP3; RP3; RP3; RP3; RP3	1327 332 336 336 336 333 332 332 332 332 332
Lapaz pr. metinf zoutonauko ji t Lapaz pr. Constraints proutonauko ji t Lapaz prmetIRF3_INGAAANYGAAACY repr Lapaz e.gr., metIRF3_INGAAANYGAAACY repr Lapaz e.gr., metIRF3_INGAAANYGAAACY repr Lapaz e.gr., metIRF3_INGAAANYGAAACYOBD Lapaz e.gr., metIRF3_INGAAANYGAAACYOBD Lapaz e.gr., metIRF3_INGAAANYGAAACYInfe Lapaz e.gr., metIRF3_INGAANYGAAACYInfe Lapaz e.gr., metIRF3_INGAANYGAAACYInfe Labaz e.gr., metIRF3_INGAANYGAAACYInfe Labaz e.gr., metIRF3_INGAANYGAAACYInfe Labaz e.gr., metIRF3_INGAANYGAAACYInfe Labaz e.gr., metIRF3_INGAANYGAAACYI Lapaz e.gr., metIRF3_INGAANYGAAACYI Lapaz e.gr.,NO2035 Lapaz e.gr., metIRF3_INGAANYGAAACYI Lapaz e.gr.,NO2035 Lapaz e.gr.,NO2035 Lapaz e.gr.,NO2035 Lapaz e.gr.,NO2035 Lapaz e.gr.,NO2035 Lapaz e.gr.,NO2036 LapageTFINKTIACTANIN LapadeIFFINKTIACTANIN	Mr 2 Source Mr 3 Source Mr 4 Source Mr 5 Source Mr 7 Source <t< td=""><td>1 1</td><td>1327 3327 336 336 335 335 335 334 334 334 334 334</td></t<>	1 1	1327 3327 336 336 335 335 335 334 334 334 334 334
Lapaz erg, meth JHYLOUKONAUKAS JL Lapaz erg, meth JHYLOUKONAUKAS JL Lapaz erg, meth JHYNIGAAKYGAAKCYI, FL Lapaz erg, meth JHYNIGAAKYGAAKCYI, epg Lapaz erg, meth JHYNIGAAKYGAAKSYI, epg Lapaz erg, meth JHYNIGAAKYGAAKSYI, epg discordsPOLIAZBICSBOORULm4 Lapade erg, meth JHYNIGAAKSIGAAKSYI, FL, repr Lapaze erg, meth JHYNIGAAKSIGAAKSYI, FL, meth Lapaze erg, meth JHYNIGAAKSIGAAKSYI, FL, meth Labaz M6024 LandresNO02555 LiffinITVDMIMO000011 LifkbpM6036 LifkpM5036 LifkpM5036 LifkpM5037 LaborrdbJHYENCSMOOFEGL 1m1 LandresNO2280 Lapaze erg,NO7412 LifkpM5776 LifkpM576 LifkpM576 LifkpM576 LifkpM576 LifkpM576 LifkpM576 LifkpM576 LifkpM576 LifkpM57	MAY 20 (directAnostation). MP2 9 (directAnostation). MP3 19 (directAnostation).	BP111021 BP11102111011021 BP1110211101101101101101101101101011010	137 137 137 137 138 139 136 135 135 135 135 137 132 132 132 132 132 132 132 132
Lippid cyt, meth	MAY EXAMPLATION OF A Comparison of the second secon	1 1 1	1327 1327 1327 1327 1328 1329 1339 1
Lapaz erg, meth JIN 2, TUNOVANUMOS 24 Lapaz erg, meth JIN 2, TUNOVANUMOS 24 Lapaz erg, meth JIN 3, MIGAANYGAAACYI pr Lapaz erg, meth JIN 3, M	More and a second	101 102:107:107:107:00 101 101:107:107:00 101 101:107:107:00 101 101:107:107:00 101 101:107:107:00 101 101:107:107:107:00 101 101:107:107:107:107:107:107:00 101 101:107:107:107:107:107:107:107:107:107:	1327 337 336 336 335 335 335 334 334 334 334 332 332 332 332
Lippid cyt, meth. Jirk _ TouSon Nukos 24 Lippid cyt, meth. Jirk _ TouSon Nukos 24 Lippid cyt, meth. Jirk Jirk NGAAKYGAAKYK _ FL Lippid cyt, meth. Jirk Jirk AKKGAAKSKA _ OBD Lippid cyt, meth. Jirk Jirk AKKGGAAKSKA _ Cyt Lippid cyt, meth. Jirk Jirk AKKGGAAKSKA _ Lippid Lippid cyt. Jirk _ Lippid cyt Jirk _ Lippid cyt Jirk _ Lippid Lippid cyt. Jirk _ Lippid cyt Jirk _ Lippid cyt Jirk _ Lippid Lippid cyt. Jirk _ Lippid cyt Jirk _ Jirk	Mark 2002 (Minechanotation). MP3 (Minec	No.1, NP2, (187), (18	1327 1327 1327 1328 1329 1339
Lapaze pro, mem. Jin Z., Jouron Junos J. L. Lapaze pro, London J. L. Lapaze J. Lapaze	Mr L giorcumulation). Mr 2 glinet/Annotation). Mr 2 glinet/Annotation). Mr 3 glinet/Annotation). Mr 3 glinet/Annotation). Mr 3 glinet/Annotation). Mr 3 glinet/Annotation). Mr 3 glinet/Annotation). Mr 4 glinet/Annotatio	1 1 1	1327 337 336 336 335 335 335 334 334 334 332 332 332 332 332

Table S8: Cortical Microglia output from RCisTarget for premutation vs. control comparison.

motif			
	TF_highConf	TF_lowConf	NES
		ARID3A; BACH1; BACH2; EP300; FOS; FOSB; FOSL1; FOSL2; JUN; JUNB; JUND; MAF; MAFB; MAFF;	
jasparMA0501.1	NFE2 (directAnnotation).	MAFG; MAFK; NFE2L1; NFE2L2; NFE2L3 (inferredBy_MotifSimilarity).	5.34
		BACH1; BACH2; FOS; FOSB; FOSL1; FOSL2; JUN; JUNB; JUND; MAF; MAFB; MAFF; MAFG; MAFK;	
factorbookNFE2	NFE2 (directAnnotation).	NFE2L1; NFE2L2; NFE2L3 (inferredBy_MotifSimilarity).	5.05
		BACH1; BACH2; FOSL2; MAF; MAFB; MAFF; MAFG; MAFK; NFE2L1; NFE2L2; NFE2L3	
cisbpM4629	NFE2 (directAnnotation).	(inferredBy_MotifSimilarity).	4.92
		BACH2; EP300; FOS; FOSB; FOSL1; FOSL2; JUN; JUNB; JUND; MAF; MAFB; MAFF; MAFG; MAFK;	
dbcorrdb_BACH1_ENCSR000EGD_1_m1	BACH1 (directAnnotation).	NFE2; NFE2L1; NFE2L2; NFE2L3 (inferredBy_MotifSimilarity).	4.82
		BACH1; BACH2; FOS; FOSB; FOSL1; FOSL2; JUN; JUNB; JUND; MAF; MAFB; MAFF; MAFG; MAFK;	
dbcorrdb_NFE2_ENCSR000FAF_1_m1	NFE2 (directAnnotation).	NFE2L1; NFE2L2; NFE2L3 (inferredBy_MotifSimilarity).	4.75
		ARID3A; BACH2; EP300; FOS; FOSB; FOSL1; FOSL2; JUN; JUNB; JUND; MAF; MAFB; MAFF; MAFG;	
homerAWWNTGCTGAGTCAT_Bach1	BACH1 (directAnnotation).	MAFK; NFE2; NFE2L1; NFE2L2; NFE2L3 (inferredBy_MotifSimilarity).	4.65
		BACH1; BACH2; FOS; FOSB; FOSL1; FOSL2; JUN; JUNB; JUND; MAF; MAFB; MAFF; MAFG; MAFK;	
hocomocoNFE2_MOUSE.H11MO.0.A		NFE2; NFE2L1; NFE2L2; NFE2L3 (inferredBy_MotifSimilarity).	4.64
		BACH1: BACH2: FOS: FOSR: FOSI 1: FOSI 2: IUN: IUNR: IUND: MAF: MAFR: MAFR: MAFG: MAFK:	
		NEF211: NEF212: NBF1 (inferred By MotifSimilarity) MAFA	
cishn M3617	NEE2 (directAnnotation)	(inferredBy MotifSimilarity n Orthology)	4.64
		FOX13 (inferredBy_MotifSimilarity)_FOXC2: FOXD1: FOXD2: FOXD3: FOXD4: FOXD4: 1:	
cishp_M6010	FOXC1 (inferredBy, Orthology)	FOXD4L3: FOXD4L4: FOXD4L5: FOXD4L6 (inferredBy MotifSimilarity n. Orthology)	4.54
		BACH1: BACH2: EOS: EOSB: EOSI 1: EOSI 2: ILIN: ILINE: ILINE: MAEE: MAEE: MAEE: MAEC: MAEK:	
becomerce NE2L2 HUMAN H11MO 0 A	NEE2L2 (directAppotation)	NEC2: NEC211: NEC212 (inferred By Matifismilarity)	4 49
		BACH1: BACH2: EOS: EOSB: EOSI 1: EOSI 2: IUN: IUND: IUND: MAE: MAEE: MAEE: MAEC: MAEK:	-11-12
isroar M40150.2	NEE2L3 (inferred By Ortholom)	NEC1: NEC11: NEC112 (inforcedby Matifimilarity)	4.49
Jashar_www.rso.z	Ni czcz (interedby_orchology).	FOYC2: FOYD3: FOYD3: FOYD3: FOYD4: FOYD4! 3: FOYD4! 3: FOYD4! 4: FOYD4! 5: FOYD4! 6	4.40
tainale Forst DBD BTAAAVA rens	EQYC1 (inferredBy: Orthology)	(inforcedBy, MatifCimilarity, p. Orthology)	4 45
tapare_roxci_bbb_knowing_repr	roxer (meneuby_orthology).	PACHS, BACHS, FOC, FOCE S, FOCE S, FOCE S, HIN, HIND, HIND, MAC, MACD, MACC, M	4.45
hosomoso NEE2 HUMAN H11MO 0 A	NEE2 (directAppotntion)	BACH1; BACH2; FUS; FUSB; FUSL1; FUSL2; JUN; JUNB; JUNU; MAF; MAFB; MAFF; MAFG; MAFK; NEE211, NEE212, NEE212, (information, MathGranitation)	4.24
NDCOINDCO_NPE2_POWMAN.H11WIO.0.A	NPE2 (direct/millotation).	NFEZEI, NFEZEZ, NFEZES (INTERPODY_WOOTSIMILATELY).	4.34
homes UTCCTCACTCAT N=D	NEE2L2 (direct Approximation)	BACH1; BACH2; FOS; FOSB; FOSL1; FOSL2; JUN; JUNB; JUND; MAF; MAFB; MAFF; MAFG; MAFK;	4.24
Initial_HIGCIGAGICAT_NI12	NPE2L2 (unectamotation).	NFE2; NFE2LI; NFE2LS; TCFI2 (Interreuby_motifsininarity).	4.54
homer GATGACTCAGCA NE 52	NEC2 (directAppotation)	BACH1; BACH2; EP300; FOS; FOSB; FOSL1; FOSL2; JUN; JUNB; JUND; MAF; MAFA; MAFB; MAFF; MAEG; MAEV; MEEDA; MEED1: NEED1: 2: MEED1: 2: MAED1: 2: MAED1: 2: MAED1: 2: MEED1: 2: MAED1: 2: MAED1: 2: MAED1: 2: MAED1: 2: MEED1: 2: MEED	
nomer_GATGACTCAGCA_NF-E2	INFE2 (directAnnotation).	WARDS; WARDS; WEFZA; NFEZLI; NFEZLI; NFEZLI3 (InferredBy_MotifSimilarity).	4.34
	NECO 2 (-foredBy Orthology)	BACH1; BACH2; FOS; FOSB; FOSL1; FOSL2; JUN; JUNB; JUND; MAF; MAFB; MAFF; MAFG; MAFK;	
CISDD	NFE2L2 (InterredBy_Orthology).	NFE21 NFE2L1; NFE2L3 (InterredBy_Motifsimilarity).	4.21
Jaspar_mAU555.1		SKE (Interredby_Motifsimilarity_n_Orthology).	4.15
cisbp_M2348		SRF (InterredBy_MotifSimilarity_n_Orthology).	4.12
		FOXC2; FOXD2; FOXD3; FOXF1; FOXF2; FOXG1; FOXI1; FOXJ1; FOXJ2; FOXK1; FOXL1; FOXN2;	
		FOXO1; FOXO3; FOXO4; FOXP1; FOXP2; FOXP3; FOXQ1 (inferredBy_MotifSimilarity). FOXD1;	
		FOXD4; FOXD4L1; FOXD4L3; FOXD4L4; FOXD4L5; FOXD4L6; FOXI2; FOXI3; FOXK2; FOXL2;	
cisbp_M6016	FOXJ3 (inferredBy_Orthology).	FOXN3; FOXO6; FOXP4 (inferredBy_MotifSimilarity_n_Orthology).	4.09
		BACH1; BACH2; FOSL1; MAF; MAFB; MAFF; MAFG; MAFK; NFE2; NFE2L1; NRF1	
transfac_proM03835	NFE2L2 (directAnnotation).	(inferredBy_MotifSimilarity).	4.08
		GTF2F1; NELFE; POLR2A; TAF1; TBP (inferredBy_MotifSimilarity). TBPL2	
dbcorrdb_GTF2B_ENCSR000DOE_1_m1	GTF2B (directAnnotation).	(inferredBy_MotifSimilarity_n_Orthology).	4.04
		FOXC2; FOXD2; FOXF1; FOXF2; FOXG1; FOXI1; FOXJ1; FOXJ2; FOXK1; FOXL1; FOXN2; FOXO1;	
		FOXO3; FOXO4; FOXP1; FOXP2; FOXP3; FOXQ1 (inferredBy_MotifSimilarity). FOXA2; FOXD1;	
		FOXD3; FOXD4; FOXD4L1; FOXD4L3; FOXD4L4; FOXD4L5; FOXD4L6; FOXI2; FOXI3; FOXK2;	
taipale_Foxj3_DBD_RTAAACAA	FOXJ3 (inferredBy_Orthology).	FOXL2; FOXN3; FOXO6; FOXP4 (inferredBy_MotifSimilarity_n_Orthology).	3.98
		AR; FOXA1; NR3C1 (inferredBy_MotifSimilarity). PGR	
cisbpM5684	NR3C2 (directAnnotation).	(inferredBy_MotifSimilarity_n_Orthology).	3.98
		GTF2B: GTF2F1: POLR2A: TAF1 (inferredBy_MotifSimilarity), TBPL2	
swissregulon hs TBP.p2	TBP (directAnnotation).	(inferredBy MotifSimilarity n Orthology).	3.96
		AR: FOXA1: NR3C2: PGR (inferredBy MotifSimilarity), HSE1: HSE2: HSE4	
cisbp M1935	NR3C1 (inferredBy Orthology).	(inferredBy MotifSimilarity n Orthology).	3.93
cisbp M5683	NR3C1 (directAnnotation).	AR: FOXA1: NR3C2: PGR (inferredBy_MotifSimilarity).	3.9
tainale AB full BRGWACANNNTGTWCYY	AB (directAppotation)	NB3C1: NB3C2 (inferredBy_MotifSimilarity)	3.88
	Parte Bande Banden	AR: EQXA1: PGR (inferredBy, MotifSimilarity) HSE1: HSE2: HSE4	
cishp M4440	NB3C1 (direct Appotation)	(inferredBy_MotifSimilarity_n_Orthology)	3.88
tainala NR3C1 DRD NRGWACANNNTGTWCYN	NB3C1 (direct Apportation)	AD: EOXA1: ND2C2: PGB (inferredBy, MotifSimilarity)	3.99
talpare_wrsc1_bbb_wrdwwcanninitiwchi	wisci (directamotation).	POYA1, ND3C1, DCD (inferredby, Mehl@imlinainty).	5.00
side MG143	AD (direct Association)	/informadity, Matificializity, a Onthelemy)	2.05
C130PM0142	Ar (unecomotation).	(mereosy_woodsimilarity_in_ordiology).	3.05
		BACH1; BACH2; FOS; FOSB; FOSE1; FOSE2; JUN; JUNB; JUND; MAF; MAFB; MAFF; MAFG; MAFK;	
and second as the MERT of		NFEZLI; NFEZLZ; NKFI (InterredBy_Motifsimilarity). MAFA	2.05
swissregulon_ns_NFE2.p2	NFE2 (directAnnotation).	(InterreoBy_MotifSimilarity_n_Orthology).	3.85
cisbp_M5289	AR (directAnnotation).	NR3C1; NR3C2 (inferredBy_MotifSimilarity).	3.84
yetrascotmku42w_1483	SRF (InterredBy_Orthology).		3.85
		GTE2B; GTE2E1; POLRZA; TAE1 (interredBy_MotifSimilarity). TBPL2	
cisbp_M4010	TBP (directAnnotation).	GIT2B; GIT2F1; POLKZA; TAF1 (interredBy_Motifsimilarity). TBPL2 (inferredBy_MotifSimilarity_n_Orthology).	3.82
cisbp_M4010	TBP (directAnnotation).	GTE2B; GTE2F1; POLR2A; TAF1 (Interredby_MotifSimilarity), TBPL2 (inferredby_MotifSimilarity,_Orthology), GTF2B; GTF2F1; POLR2A; TAF1; TBP (inferredby_MotifSimilarity), TBPL2	3.82
cisbpM4010 jasparM40108.2	TBP (directAnnotation).	G124;5;6124;2;VOLK24; (h42) (interredby_MottSmillarity), TBPL2 (inferredby_MottISimillarity_n_Orthology), G128;G125;2;FOL824;745;1;B9 (inferredBy_MottISimillarity), TBPL2 (inferredBy_MottISimillarity_n_Orthology).	3.82
cisbp_M4010 jsspar_M40108.2	TBP (directAnnotation).	G1r24; 61r21; PUXIAX, IA2 Interedely_MotiSimilarity), IBPL2 (inferredly_MotiSimilarity, _OTHology), G1r28; G1r2F1; PUXIA2, IA21; IBP (inferredBy_MotifSimilarity), TBPL2 (inferredBy_MotiSimilarity, _OTHology), G1r28; G1r2F1; NLEEE (inferredBy_MotiSimilarity), TBPL2	3.82
cisbp_M4010 jispar_M40108.2 factorbook_TBP	TBP (directAnnotation). POLR2A; TAF1; TBP (directAnnotation).	G1r24; 61r21; PUCKAK, IA3 (Interedely_Motifismilarity), IBPL2 (inferredely_MotifismilarityO_Thology), GTF28; GTF2F1; POLR2A; TAF1; T8P (inferredely_Motifismilarity), T8PL2 (inferredely_MotifismilarityO_Thology), GTF28; GTF2F1; PUEFE (inferredely_Motifismilarity), T8PL2 (inferredely_MotifismilarityO_Thology),	3.82 3.8 3.78
cisbp_M4010 jsipar_M40108.2 factorbook_TBP	TBP (directAnnotation). POLR2A; TAF1; TBP (directAnnotation).	Gir24; 6:142; FVDUKAK, 142; Interedely_MottSimiliarity), 1842 (inferredly_MottSimiliarity,OFUDIology), GTF26; 6:1725; PVDUR2A; 142; 1389 (inferredly_MottSimiliarity), TBPL2 (inferredly_MottSimiliarity,OFUDIology), GTF26; 6:1725; NUELFE (inferredly_MottSimiliarity), TBPL2 (inferredly_MottSimiliarity,OFUDIology), Ak; FOXA; 1943CL (inferredly_MottSimiliarity), FGR	3.82 3.8 3.78
cisbp_M4010 jsspar_M40108.2 factorbook_TBP taipale_NR3C2_DBD_NRGNACANNNTGTNCYN	TBP (directAnnotation). POLR2A; TAF1; TBP (directAnnotation). NR3C2 (directAnnotation).	Gir24; Gir25; PUCKAK, IA3: Interedely_MottSimilarity), IBPL2 (inferredly_MottSimilarity_n_Orthology). GTR28; GTR21; PD(R2A, TAF2; T8P [inferredBy_MottISimilarity], T8PL2 (inferredBy_MottISimilarity_n_Orthology). GTR28; GTR21; NRE1{ (inferredBy_MottISimilarity], T8PL2 (inferredBy_MottISimilarity_n_Orthology). AR; FOXAI; NRS1 (inferredBy_MottISimilarity), PGR (inferredBy_MottISimilarity_n_Orthology).	3.82 3.8 3.78 3.77
cisbp_M4010 jispar_M40108.2 factorbook_TBP taipale_NR3C2_DBD_NRGNACANNNTGTNCYN	TBP (directAnnotation). POLR2A; TAF1; TBP (directAnnotation). NR3C2 (directAnnotation).	Gir24; 6:172; FUXURAF, IAP L (Interedely_MottSimilarity), IBPL2 (interedely_MottSimilarity, _ DFUAP, MottSimilarity), TBPL2 (interedely_MottSimilarity, _ DFUAP, _ D	3.82 3.8 3.78 3.77
cisbp_M4010 jsspar_M40108.2 factorbook_TBP taipale_N83C2_DBD_NRGNACANNNTGTNCYN dbcorrdb_FOXA1_ENCSR0008PX_1_m1	TBP (directAnnotation). POLR2A; TAF1; TBP (directAnnotation). NR3C2 (directAnnotation). FOXA1 (directAnnotation).	Gir24; 6:1672; PUCKAK, 143: (Interedby_Motifismiliarity), 18/L2 (inferredby_Motifismiliarity,OTHology), GTF28; GTF27; PUCKAZ, 1743; 189: (inferredby_Motifismiliarity), TBPL2 (inferredby_Motifismiliarity,OTHology), GFF28; GTF27; NELFE (inferredby_Motifismiliarity), TBPL2 (inferredby_Motifismiliarity,OTHology), AR; NR3C1; NR3C2; PGR (inferredby_Motifismiliarity), HSF1; HSF2; HSF4 (inferredby_Motifismiliarity,OTHology),	3.82 3.8 3.78 3.77 3.77
cisbp_M4010 jispar_M40108.2 factorbook_TBP taipale_NR3C2_DBD_NRGNACANINITGTNCYN dbcorrdb_FOXA1_ENCSR000BPX_1_m1	TBP (directAnnotation). POLR2A; TAF1; TBP (directAnnotation). NR3C2 (directAnnotation). FOXA1 (directAnnotation).	Gir24; 6:172; PUXLAX, IA2 interredby_MottSimilarity), IBPL2 (inferredby_MottSimilarity, DFNL2)	3.82 3.8 3.78 3.77 3.77
cibp_M4010 jsspar_M40108.2 factorbook_TBP taipple_NR3C2_DBD_NRGNACANNNTGTNCYN dbcorrdb_FOXA1_ENCSR0008PX_1_m1 homer_CTATAAAAGCSY_TATA-box	TBP (directAnnotation). POLR2A; TAF1; TBP (directAnnotation). NR3C2 (directAnnotation). FOXA1 (directAnnotation).	Gir24; 6:172; FUCKAC, IAP 1, Intercedely_MottSimiliarity), IBPL2 (inferredly_MottSimiliarity, D_THOLOgy), GTF28; 6:1725; FUCKA2, IAP1; TBP (inferredly_MottSimiliarity), TBPL2 (inferredly_MottSimiliarity, D_THOLOgy), GTF28; GTF27; NELFE (inferredly_MottSimiliarity), TBPL2 (inferredly_MottSimiliarity, D_THOLOgy), GFF28; GTF27; NELFE (inferredly_MottSimiliarity), FGR (inferredly_MottSimiliarity, D_THOLOgy), GFF28; GTF27; NELFE (inferredly_MottSimiliarity), FGR (inferredly_MottSimiliarity, D_THOLOgy), POLR24, TAF1; TBP (inferredly_MottSimiliarity), FBF1; HSF2; HSF4 (inferredly_MottSimiliarity, D_THOLOgy), POLR24, TAF1; TBP (inferredly_MottSimiliarity), TBPL2 (inferredly_MottSimiliarity, D_THOLOgy),	3.82 3.8 3.78 3.77 3.77 3.76
cisbp_M4010 jsspar_M40108.2 factorbook_TBP taipale_NR3C2_DBD_NRGNACANINITGTNCYN dbcorrdb_FOXA1_ENCSR000BPX_1_m1 homer_CTATAAAAGCSV_TATA-box	TBP (directAnnotation). POLR2A; TAF1; TBP (directAnnotation). NR3C2 (directAnnotation). FOXA1 (directAnnotation).	Gir24; 6:172; FUOLKAF, IAP L (Interedely_MottSimiliarity), IBPL2 (interedely_MottSimiliarity, _DFUAL (interedely_MottSimiliarity), _DFUAL (interedely_MottSimiliarity, _DFUAL (interedely_MottSimiliarity), _DFUAL (in	3.82 3.8 3.78 3.77 3.77 3.76
cisbp_M4010 jsspar_M40108.2 factorbook_TBP taipale_NR3C2_DBD_NRGNACANNITGTINCYN dbcorrdb_FOXA1_ENCSR000BPX_1_m1 homer_CTATAAAAGCSV_TATA-box cisbp_M6367	TBP (directAnnotation). POLR2A; TAF1; TBP (directAnnotation). NR3C2 (directAnnotation). FOXA1 (directAnnotation). NFE2 (directAnnotation).	Gir24; 6:172; FUCKAC, K42; Interedely_MotifSmilarity), IBPL2 (inferredely_MotifSmilarity, D_THOLOgy), GTF26; CIF2F1; PDCR2A; T473; I38P (inferredely_MotifSmilarity), TBPL2 (inferredely_MotifSmilarity, D_THOLOgy), GTF26; CIF2F1; NELFE (inferredely_MotifSmilarity), TBPL2 (inferredely_MotifSmilarity), DFR12 (inferredely_MotifSmilarity), DFR2 (inferredely_MotifSmilarity), DFR3	3.82 3.8 3.78 3.77 3.77 3.77 3.76 3.75
cisbp_M4010 isspar_MA0108.2 factorbook_TBP taipale_NR3C2_DBD_NRGNACANINITGTNCYN dbcorrdb_FOXA3_ENCSR000BPX_1_m1 homer_CTATAAAAGCSV_TATA-box cisbp_M6367 elemento_GCGCCCC	TBP (directAnnotation). POLR2A; TAF1; TBP (directAnnotation). NR3C2 (directAnnotation). FOXA1 (directAnnotation). NFE2 (directAnnotation).	Gir24; 6:172; FOUKACA, IV32; Interredely_MottISmiliarity), IBPL2 (inferredely_MottISmiliarity, DFNL2 (inferredely_MottISmiliarity, DFNL2 (inferredely_MottISmiliarity, TBPL2 (inferredely_MottISmiliarity, TBPL2 (inferredely_MottISmiliarity, TBPL2 (inferredely_MottISmiliarity, DFNL2 (inferredely_MottISmiliarity, DFNL (inferredely_MottISmiliarity,	3.82 3.8 3.78 3.77 3.77 3.76 3.76 3.75 3.73
cibbp_M4010 jsspar_M40108.2 factorbook_TBP taipale_NR3C2_DBD_NRGNACANNITGTINCYN dbcorrdb_FOXA1_ENCSR000BPX_1_m1 homer_CTATAAAAGCSV_TATA-box cisbp_M6367 elemento_GCGGCGCC	TBP (directAnnotation). POLR2A; TAF1; TBP (directAnnotation). NR3C2 (directAnnotation). FCXA1 (directAnnotation). NFE2 (directAnnotation).	Gi124; 6:1672; PUCKAK, IAP 1, Interredby_MottSimilarity), IBPL2 (interredby_MottSimilarity,_Othology), GT28; 6:1725; PUCKAX, IAP3; IBP (interredby_MottSimilarity), TBPL2 (interredby_MottSimilarity,_Othology), GT28; 6:1725; NLFE (interredby_MottSimilarity), TBPL2 (interredby_MottSimilarity,_Othology), AR; FOXA1; NR3C1 (inferredby_MottSimilarity), PGR (interredby_MottSimilarity,_Othology), AR; NR3C1; NR3C2; RGR (interredby_MottSimilarity), IBF1; ISF2; ISF4 (interredby_MottSimilarity,_Othology), AB; FOXA1; NR3C1; RGP, GRR (interredby_MottSimilarity), TBPL2 (interredby_MottSimilarity,_Othology), AB; FOXA1; NR3C1; RGP; GRR (interredby_MottSimilarity), TBPL2 (interredby_MottSimilarity,_Othology), ABCH1; BACH2; FOSB; FOS1; IOS2; JUN3; JUN8; JUN9; MAF; MAF6; MAF6; MAF6; MFE2; INF2L1; NF2L2; (interredby_MottSimilarity), BACH1; BACH2; EP300; JUN; MAF; MAF6; MAF6; NFE2; NFE2L1 (interredby_MottSimilarity), BACH1; BACH2; EP300; JUN; MAF; MAF6; MAFK; NFE2; NFE2L1 (interredby_MottSimilarity), BACH1; BACH2; EP300; JUN; MAF; MAF6; MAFK; NFE2; NFE2L1 (interredby_MottSimilarity), BACH1; BACH2; EP300; JUN; MAF; MAF6; MAFK; NFE2; NFE2L1 (interredby_MottSimilarity), BACH1; BACH2; EP300; JUN; MAF; MAF6; MAF6; MAF6; MFE2; NFE2L1 (interredby_MottSimilarity), BACH1; BACH2; EP300; JUN; MAF; MAF6; MAF6	3.82 3.8 3.78 3.77 3.77 3.76 3.75 3.73
cisbp_M4010 isspar_MA0108.2 factorbook_TBP taipale_NR3C2_DBD_NRGNACANINITGTNCYN dbcorrdb_FOXA3_ENCSR000BPX_1_m1 homer_CTATAAAAGCSV_TATA-box cisbp_M6367 elemento_GGGGCCC transfac_pro_M02263	TBP (directAnnotation). POLR2A; TAF1; TBP (directAnnotation). NR3C2 (directAnnotation). FXXA1 (directAnnotation). NFE2 (directAnnotation). NFE2 (directAnnotation). NFE2L2 (directAnnotation).	Gi123; 6:12-12; POURAC, IV3 L Interredely_MottSimiliarity), IBPL2 (inferredely_MottSimiliarity, D_FNL2 (inferredely_MottSimiliarity, D_FNL2 (inferredely_MottSimiliarity, D_FNL2 (inferredely_MottSimiliarity, DFNL2 (inferredely_MottSimiliarity), DFNL (inferredely_MottS	3.82 3.8 3.78 3.77 3.77 3.77 3.76 3.75 3.73 3.64
cisbp_M4010 jsipar_M40108.2 factorbook_TBP taipale_NR3C2_DBD_NRGNACANNITGTNCYN dbcorrdb_FOXA1_ENCSR000BPX_1_m1 homer_CTATAAAAGCSV_TATA-box cisbp_M6367 elemento_GCGCGCC transfac_pro_M02263	TBP (directAnnotation). POLR2A; TAF1; TBP (directAnnotation). NR3C2 (directAnnotation). FOXA1 (directAnnotation). NFE2 (directAnnotation). NFE2L2 (directAnnotation).	Gi124; 6:172; PUCKAX, IA2; Intercedely_MottSimilarity), IBPL2 (inferredely_MottSimilarity, _ DFUCkay, IA2; IB2) (inferredely_MottSimilarity, _ TB12) (inferredely_MottSimilarity, _ TB12) (inferredely_MottSimilarity, _ TB12) (inferredely_MottSimilarity, _ TB12) (inferredely_MottSimilarity, _ TB12	3.82 3.8 3.78 3.77 3.77 3.77 3.76 3.75 3.73 3.64
cisbp_M4010 isspar_M40108.2 factorbook_TBP taipale_NR3C2_DBD_NRGNACMINITGTNCYN dbcorrdb_FOXA1_ENCSR000BPX_1_m1 homer_CTATAAAAGCSV_TATA-box cisbp_M6367 elemento_GCGGCCC transfac_pro_M02263 dbcorrdb_GTT2F1_ENCSR000EHC_1_m1	TBP (directAnnotation). POLR2A; TAF1; TBP (directAnnotation). NR3C2 (directAnnotation). FXXA1 (directAnnotation). NFE2 (directAnnotation). NFE2 (directAnnotation). GTF2F1 (directAnnotation).	Gi123; 6:12-12; POURAC, IAP 1, Interredby_MottSimiliarity), IBPL2 (inferredby_MottSimiliarity, D_FNL2 (inferredby_MottSimiliarity), DNL2 (3.82 3.8 3.78 3.77 3.77 3.76 3.75 3.73 3.64 3.63
cisbp_M4010 isipar_M40108.2 factorbook_TBP taipale_NR3C2_DBD_NRGNACANNITGTINC'N dbcorrdb_FOXA1_ENCSR000BPX_1_m1 homer_CTATAAAAGCSV_TATA-box cisbp_M4387 elemento_GCGCGCC transfac_pro_M02263 dbcorrdb_GTF2F1_ENCSR000EHC_1_m1	TBP (directAnnotation). POLR2A; TAF1; TBP (directAnnotation). NR3C2 (directAnnotation). FOXA1 (directAnnotation). NFE2(directAnnotation). NFE2L2 (directAnnotation). GTT2F1 (directAnnotation).	Gi124; 6:172; PUCKAX, IA2; Interredby_MottSimilarity), IBPL2 (inferredby_MottSimilarity, D_thology), GTF28; 6:TF21; PUCKAX, IA23; IBP (inferredby_MottSimilarity), TBPL2 (inferredby_MottSimilarity, D_thology), GTF28; 6:TF21; RUEF (inferredby_MottSimilarity), TBPL2 (inferredby_MottSimilarity, D_thology), AR; FOXAI, INBSCI (inferredby_MottSimilarity), FGR (inferredby_MottSimilarity, D_thology), AR; ROXAI, INBSCI (inferredby_MottSimilarity), TBPL2 (inferredby_MottSimilarity, D_thology), AR; ROXAI, INBSCI (inferredby_MottSimilarity), TBPL2 (inferredby_MottSimilarity, D_thology), AR; ROXAI, INBSCI (inferredby_MottSimilarity), TBPL2 (inferredby_MottSimilarity, D_thology), ARCH1; BACH2; FOSO; ROS; ROSI, FOSI, FO	3.82 3.8 3.78 3.77 3.77 3.77 3.76 3.75 3.73 3.64 3.63
cibp_M4010 jsspar_M40108.2 factorbook_TBP taipale_NR3C2_DBD_NRGNACANNNTGTNCYN dbcorrdb_FOXA1_ENCSR000BPX_1_m1 homer_CTATAAAAGCSV_TATA-box cisbp_M6367 elemento_GCGCGCC transfac_pro_M02263 dbcorrdb_GTF2F1_ENCSR000EHC_1_m1	TBP (directAnnotation). POLR2A; TAF1; TBP (directAnnotation). NR3C2 (directAnnotation). FXXA1 (directAnnotation). NFE2 (directAnnotation). NFE212 (directAnnotation). GTF2F1 (directAnnotation).	Gir2di, Gir2di, POLKAA, IAP L Interredely, MottiSmiliarity), IBPL2 (interredely, MottiSmiliarity, D-THOLOGY), Gir72di, Gir72di, POLKAA, TAPJ, IBP (interredely, MottiSmiliarity), TBPL2 (interredely, MottiSmiliarity, D-THOLOGY), Gir72di, Gir72di, NCLEE (interredely, MottiSmiliarity), TBPL2 (interredely, MottiSmiliarity, D-THOLOGY), AR, FOXAJ, NRSCI (interredely, MottiSmiliarity), TBPL2 (interredely, MottiSmiliarity, D-THOLOGY), AR, ROXAJ, NRSCI (interredely, MottiSmiliarity), TBPL2 (interredely, MottiSmiliarity, D-THOLOGY), AR, ROXAJ, NRSCI (interredely, MottiSmiliarity), TBPL2 (interredely, MottiSmiliarity, D-THOLOGY), AR, ROXAJ, NRSCI (interredely, MottiSmiliarity), TBPL2 (interredely, MottiSmiliarity, D-THOLOGY), ARALLI, BACH2; FOS; FOSB; FOSL1; FOSL2; JUN; JUNB; JUND; MAF; MAFB; MAFF; MAFG; MAFK; NFE2L1, NFE2L3; NFE2L3 (interredely, MottiSmiliarity), ARAH1; BACH2; FOS; FOSB; FOSL1; FOSL2; JUN; JUNB; JUND; MAF; MAFB; MAFF; MAFG; MAFK; NFE2L4; MFE2L3; TBP (interredely, MottiSmiliarity), GIF28; BALFF; POLR23; TAF1; TBP (interredely, MottiSmiliarity), GIF28; BALFF; POLR23; TAF1; TBP (interredely, MottiSmiliarity), FOXC2; FOXD2; FOXF1; FOXZ2; FOXG3; FOXL1; FOXD1; FOXD2; FOXX1; FOXD1; FOXD2; FOXX1; FOXD1; FOXD2; FOXX1; FOXD1; FOXD44;	3.82 3.8 3.78 3.77 3.77 3.77 3.76 3.75 3.73 3.64 3.63
cisbp_M4010 isispar_M40108.2 factorbook_TBP taipale_NR3C2_DBD_NRGNACANNITGTINCYN dbcorrdb_FOXA1_ENCSR000BPX_1_m1 homer_CTATAAAAGCSV_TATA-box cisbp_M45367 elemento_GCGCGCC transfac_pro_M02263 dbcorrdb_GT72F1_ENCSR000EHC_1_m1	TBP (directAnnotation). POLR2A; TAF1; TBP (directAnnotation). NRB2C2 (directAnnotation). FOXA1 (directAnnotation). NFE2 (directAnnotation). NFE2L2 (directAnnotation). GTE2F1 (directAnnotation).	Gi124; 6:1721; PUXLAX, IA3: Interredby_MottISimilarity), IBYL2 (inferredby_MottISimilarity, D-Thology), GTF28; GTF21; PDXRAX, TA73; IB9 (inferredby_MottISimilarity), TBPL2 (inferredby_MottISimilarity, D-Thology), GTF28; GTF21; NELFE (inferredby_MottISimilarity), TBPL2 (inferredby_MottISimilarity, D-Thology), AR; FOXAI, INBSC1 (inferredby_MottISimilarity), FGR (inferredby_MottISimilarity, D-Thology), AR; ROXAI, INBSC2; FGR [inferredby_MottISimilarity], TBPL2 (inferredby_MottISimilarity, D-Thology), AR; ROXAI, INBSC2; FGR [inferredby_MottISimilarity], TBPL2 (inferredby_MottISimilarity, D-Thology), ARCH1; BACH2; FGSR5; GSR5; FGSL1; FGSL2; UNIV, INBS; UNID; MAF; MAFB; MAFF; MAFG; MAFK; NFE2L1; NFE2L3 (inferredby_MottISimilarity), BCAH1; BACH2; FGS0; FGSL5; TGSL1; FGSL2; UNIV, INB; UNID; MAF; MAFB; MAFF; MAFG; MAFK; NFE2L1; NFE2L3 (inferredby_MottISimilarity, D-Thology), BCAH; BACH2; FGS0; FGSL5; TGSL1; FGSL2; FGSL2; UNIV, INB; UNID; MAF; MAFB; MAFF; MAFG; MAFK; NFE2L1; NFE2L3 (inferredby_MottISimilarity, D-Thology), BCAH; BACH2; FGSD2; UNIX, MAF; MAFG; MAFK; NFE2, NFE2L1 (inferredby_MottISimilarity), BCH4; BACH2; FGSD2; UNIX, MAF; MAFG; MAFK; NFE2, NFE2L1 (inferredby_MottISimilarity, D-Thology), BCH4; BACH2; FGVC2; FGVC2; FGVC3; FG	3.82 3.8 3.78 3.77 3.77 3.77 3.76 3.75 3.73 3.64 3.63
cisbp_M4010 jsspar_M40108.2 factorbook_TBP taipple_NR3C2_DBD_NRGNACANNNTGTNCYN dbcorrdb_FOXA1_ENCSR000BPX_1_m1 homer_CTATAMAAGCSY_TATA-box cisbp_M6367 elemento_GCGGCCC transfac_pro_M02263 dbcorrdb_GTF2F1_ENCSR000EHC_1_m1 cisbp_M5460	TBP (directAnnotation). POLR2A; TAF1; TBP (directAnnotation). NR3C2 (directAnnotation). FXXA1 (directAnnotation). NFE2 (directAnnotation). NFE212 (directAnnotation). GTT2F1 (directAnnotation). FXXL1 (directAnnotation).	Gir2di; Gir2di; POLKAC, IV2 L (Interedely_MottSimilarity), IBPL2 (interedely_MottSimilarity, D_FNL2 (interedely_MottSimi	3.82 3.8 3.77 3.77 3.76 3.75 3.73 3.64 3.63 3.62
cisbp_M4010 jsspar_M40108.2 factorbook_TBP taipale_NR3C2_DBD_NRGNACANINTGTNC'N dbcorrdb_FOXA1_ENCSR000BPX_1_m1 homer_CTATAAAAGCSV_TATA-box cisbp_M5367 elemento_GCGCGCC transfac_pro_M02263 dbcorrdb_GTT2F1_ENCSR000EHC_1_m1 cisbp_M5460 transfac_pro_M01240	TBP (directAnnotation). POLR2A; TAF1; TBP (directAnnotation). NR3C2 (directAnnotation). FOXA1 (directAnnotation). NFE2 (directAnnotation). SFE212 (directAnnotation). FOXL1 (directAnnotation). GTF2F1 (directAnnotation). GTF2F1 (directAnnotation).	Gi123; 6:12-3; PUXLAX, IA3; Interredby_MotiDiamilarity), IBPL2 (inferredby_MotiBiamilarityOtherselbase), GTF28; 6:172-1; PDXRAX, TA73; IB9 (inferredby_MotiBiamilarity], TBPL2 (inferredby_MotiBiamilarity_Otherselbase), GTF28; 0:172-1; NELFE (inferredby_MotiBiamilarity], TBPL2 (inferredby_MotiBiamilarity_Otherselbase), AR; FOXAX; INB3C1 (inferredby_MotiBiamilarity], FBR2 (inferredby_MotiBiamilarity_O_Othology), AR; ROXAX; INB3C1 (inferredby_MotiBiamilarity], FBR2 (inferredby_MotiBiamilarity_O_Othology), AR; ROXAX; INB3C1 (inferredby_MotiBiamilarity], TBPL2 (inferredby_MotiBiamilarity_O_Othology), AR; ROXAX; INB3C1 (inferredby_MotiBiamilarity], TBPL2 (inferredby_MotiBiamilarity_O_Othology), AR; ROXAX; ROXE; ROSE; ROSE; IOS2; IOS2; UNN; UNR9; UNR9; MAF; MAFG; MAFF; MAFF; MAFG; MAFF; MAFF; MAFG; MAFF; MAFF; MAFG; MAFF; MAFF;	3.82 3.8 3.78 3.77 3.77 3.76 3.75 3.73 3.64 3.63 3.62 3.62
cisbp_M4010 jsspar_M40108.2 factorbook_TBP taipple_NR3C2_DBD_NRGNACANNITGTINCYN dbcorrdb_FOXA1_ENCSR000BPX_1_m1 homer_CTATAAAAGCSY_TATA-box cisbp_M6367 elemento_GCGGGCC transfac_pro_M02263 dbcorrdb_GT72F1_ENCSR000EHC_1_m1 cisbp_M5460 transfac_pro_M01240 star_STATAWARSVV	TBP (directAnnotation). POLR2A; TAF1; TBP (directAnnotation). NR3C2 (directAnnotation). FOXA1 (directAnnotation). NFE2 (directAnnotation). GTT2F1 (directAnnotation).	Gir2d; 6:1721; PUKIAA; IA2 (Interedely_MottiSimilarity), IBP12 (interedey_MottiSimilarity, D-THORP), Gir72d; 6:1721; PUKIAA; IA2; IBP (interedely_MottiSimilarity), TBP12 (interedey_MottiSimilarity, D-THORP), Gir72d; 7:1721; RUEE(interedey_MottiSimilarity), TBP12 (interedey_MottiSimilarity, D-THORP), AR; FOXAI; NB32; (interedey_MottiSimilarity), TBP12 (interedey_MottiSimilarity, D-THORP), AR; FOXAI; NB32; (interedey_MottiSimilarity), TBP12 (interedey_MottiSimilarity, D-THORP), AR; RISAI; NB32; PGR [interedey_MottISimilarity], TBP12 (interedey_MottiSimilarity, D-THORP), DCIA2A; TA2; TBP (interedey_MottISimilarity), TBP2 (interedey_MottISimilarity), TBP2 (interedey_MottISimilarity, D-THORP), AR; RISAI; BP2(interedey_MottISimilarity), BACH; IsACH2; FOS0; IOS1; FOS1; FOS1; IOS1; IUNE; UNB; UNB; MAF; MAF; MAF; MAF; MAF; MAF; MAF; MAF	3.82 3.8 3.77 3.77 3.77 3.76 3.75 3.73 3.64 3.63 3.62 3.62 3.62
cisbp_M4010 jsspar_M40108.2 factorbook_TBP taipale_NR3C2_DBD_NRGNACANINTGTNC'N dbcorrdb_FOXA1_ENCSR000BPX_1_m1 homer_CTATAAAAGCSV_TATA-box cisbp_M5367 elemento_GCGCGCC transfac_pro_M02263 dbcorrdb_GTT2F1_ENCSR000EHC_1_m1 cisbp_M5460 transfac_pro_M02263	TBP (directAnnotation). POLR2A; TAF1; TBP (directAnnotation). NR3C2 (directAnnotation). FOXA1 (directAnnotation). NFE2 (directAnnotation). SFE212 (directAnnotation). GFT2F1 (directAnnotation). GTT2F1 (directAnnotation). GTT2RID1 (directAnnotation). TBP; TBP12 (inferedBy_Othology).	Gir2di, Gir2di, Gir2di, Gir2di, Girding, Girding, Girding, Gir2di, Gir2di, Girding,	3.82 3.8 3.77 3.77 3.76 3.75 3.73 3.64 3.63 3.64 3.62 3.62 3.62 3.62
cisbp_M4010 isspar_M40108.2 factorbook_TBP taipale_NR3C2_DBD_NRGNACANNITGTINCYN dbcorrdb_FOXA1_ENCSR000BPX_1_m1 homer_CTATAAAAGCSV_TATA-box cisbp_M6367 elemento_GCGCGCC transfac_pro_M02263 dbcorrdb_GT2F1_ENCSR000EHC_1_m1 cisbp_M5460 transfac_fT70_M01240 star_STATAWAWRSVV neph_UW_M0tf0510 wisregulon_hc_FOXP3.02	TBP (directAnnotation). POLR2A; TAF1; TBP (directAnnotation). NR3C2 (directAnnotation). FOXA1 (directAnnotation). NFE2 (directAnnotation). NFE212 (directAnnotation). GTT2F1 (directAnnotation). GTT2F1 (directAnnotation). GTT2F1 (directAnnotation). TFP:TBP12 (directAnnotation). TFP:TBP12 (directAnnotation). TF0XE1 (dir	Gir2di, Gir2di, POLKAZ, IVA 1, Interredely_MottSimilarity), IBPL2 (interredely_MottSimilarity, DFNL2 (interredely_MottSimilarity), DFNL2 (interredely_MottSimilarity), DFNL2 (interredely_MottSimilarity), DFNL2 (interredely_Mot	3.82 3.8 3.77 3.77 3.77 3.76 3.75 3.73 3.64 3.64 3.63 3.62 3.62 3.62 3.59 3.59
cisbp_M4010 jsspar_M40108.2 factorbook_TBP taipale_NR3C2_DBD_NRGNACANINTGTNCYN dbcorrdb_FOXA1_ENCSR000BPX_1_m1 homer_CTATAAAAGCSV_TATA-box cisbp_M6367 elemento_GCGCGCC transfac_pro_M02263 dbcorrdb_GTF2F1_ENCSR000EHC_1_m1 cisbp_M5460 transfac_pro_M0220 stark_STATAWANRSVV neph_UW.M0105010 swisregulon_ht_FOXP3.p2 hojdi _BRM35A	TBP (directAnnotation). POLR2A, TAF1; TBP (directAnnotation). NR3C2 (directAnnotation). FOXA1 (directAnnotation). NFE2 (directAnnotation). SFE212 (directAnnotation). GFT2F1 (directAnnotation). GFT2F1 (directAnnotation). FOXL1 (directAnnotation). FOXP3 (di	Gir2di, Gir2di, POLKAA, KP3, Interedely, MottiSmilarity), IBPL2 (inferredely, MottiSmilarity, D-THOLOGY), GTF28, GTF21, DFDKRA, TAP3, IBP (inferredely, MottiSmilarity), TBPL2 (inferredely, MottiSmilarity, D-Thology), GTF28, GTF21, DELFE (inferredely, MottiSmilarity), TBPL2 (inferredely, MottiSmilarity, D-Thology), AR, FOXAL INBCC (inferredely, MottiSmilarity), TBPL2 (inferredely, MottiSmilarity, D-Thology), AR, ROXAL INBCC (inferredely, MottiSmilarity), TBPL2 (inferredely, MottiSmilarity, D-Thology), AR, ROXAL INBCC (inferredely, MottiSmilarity), TBPL2 (inferredely, MottiSmilarity, D-Thology), AR, INBCC (INFERCE), MOTSMILIARITY), TBPL2 (inferredely, MottiSmilarity), D-Thology), BACH1; BACH2; GFOSB; FOSL; IOS2; JUNU; JUNB; JUND; MAF; MAFB; MAFF; MAFG; MAFK; NFELL; INFEL2; MFEL3 (inferredely, MottiSmilarity), EACH1; BACH2; GFOSB; FOSL; IOS2; JUND; JUNB; JUND; MAF; MAFB; MAFF; MAFG; MAFK; NFEL1; INFEL2; MEEL3 (inferredely, MottiSmilarity), ETF28, MAFE; Martised, MottiSmilarity, D-Motology), BACH1; BACH2; GFOSB; FOSL; IOS2; JUND; JUNB; JUND; MAF; MAFB; MAFF; MAFG; MAFK; (inferredely, MottiSmilarity, D-Othology), GTF28, RUFE; POLR2A; TAF1; TBP (inferredely, MottiSmilarity), ETF28, RUFE; POLR2A; TAF1; TBP (inferredely, MottiSmilarity), POLR2; TAV1; FOX2; FOX0; FOX1; FOX1; FOX1; FOX2; FOX1; FOX2; FOXAL; FOXD4; FOXD44; FOXD44; FOXD444; (inferredely, MottiSmilarity, D-CThology), POLR24; TAF1 (inferredBy, MottiSmilarity), POLR24; TAF1 (inf	3.82 3.8 3.78 3.77 3.77 3.77 3.76 3.75 3.73 3.64 3.63 3.64 3.63 3.62 3.62 3.62 3.59 3.559
cisbp_M4010 isopar_M40108.2 factorbook_TBP taipale_NR3C2_DBD_NRGNACANNITGTNCYN dbcorrdb_FOXA1_ENCSR000BPX_1_m1 homer_CTATAAAAGCSV_TATA-box cisbp_M6367 elemento_GCGCGCC transfac_pro_M02263 dbcorrdb_GTF2F1_ENCSR000EHC_1_m1 cisbp_M5460 transfac_pro_M01240 staf_STATAWAWRSVV neph_UW_Motif0510 swisregulon_m_ECW33.2 hdpl_ERM35A tidimes_M000384	TBP (directAnnotation). POLR2A; TAF1; TBP (directAnnotation). NR3C2 (directAnnotation). FOXA1 (directAnnotation). NFE2 (directAnnotation). STF2R2 (directAnnotation). GTT2F1 (directAnnotation). GTT2F1 (directAnnotation). GTT2F1 (directAnnotation). STF2R2 (directAnnotation).	Gir24; 6:1721; PUKIAA; IA3 (Interedely_MotifSimilarity), IBY22 (interedey_MotifSimilarity, D-Thology), GTP28; 6:1721; PUKIAA; IA32; IB7 (Interedely_MotifSimilarity), TBP12 (interedey_MotifSimilarity, D-Thology), GTP28; 6:1721; NELEE (Interedely_MotifSimilarity), TBP12 (interedey_MotifSimilarity, D-Thology), AR; FOXAI; NB32; (Interedely_MotifSimilarity), TBP12 (interedey_MotifSimilarity, D-Thology), AR; ROXAI; NB32; (Interedey_MotifSimilarity), TBP12 (interedey_MotifSimilarity, D-Thology), AR; ROXAI; NB32; PGR (Interedey_MotifSimilarity), TBP12 (interedey_MotifSimilarity, D-Thology), POIA2A; TA31; TB7 (Interedey_MotifSimilarity), TBP12 (Interedey_MotifSimilarity, D-Thology), BACH; I; BACH2; FOS0; FOS1; FOS1; FOS1; FOS2; IVN, UMB; UMD; MAF; MAFE;	3.82 3.8 3.78 3.77 3.77 3.76 3.75 3.73 3.64 3.63 3.64 3.63 3.62 3.62 3.62 3.59 3.59 3.58 3.58
cisbp_M4010 isspar_M40108.2 factorbook_TBP taipale_NR3C2_DBD_NRGNACANINTGTNCYN dbcorrdb_FOXA1_ENCSR000BPX_1_m1 homer_CTATAAAAGCSY_TATA-box cisbp_M6367 elemento_GCGCGCC transfac_pro_M02263 dbcorrdb_GTF2F1_ENCSR000EHC_1_m1 cisbp_M5460 transfac_pro_M01240 stark_STATAWANRSYVV neph_UW.M01f0510 swissregulon_tk_EOXP3.92 hdpl_BRM35A ttdimers_M000384 eneb_UW.M01f0241	TBP (directAnnotation). POLR2A, TAF1; TBP (directAnnotation). NR3C2 (directAnnotation). FOXA1 (directAnnotation). FOXA1 (directAnnotation). STF212 (directAnnotation). GTF2F1 (directAnnotation). GTF2F1 (directAnnotation). GTF2F1 (directAnnotation). TBP; TBP12 (inferredBy_Othology). FOXP3 (directAnnotation). ESP39 (directAnnotation). IZF2; STAT1 (directAnnotation). IZF2; STAT1 (directAnnotation). IZF2; STAT1 (directAnnotation). IZF2; STAT1 (directAnnotation). IZF29; STAT1 (directAnnotation).	Gir2d; 0:1721; PUXRAY, IA91; Interredely_MotiSimilarity), IBP12 (inferredely_MotiSimilarity, D_FNL2 (3.82 3.83 3.77 3.77 3.77 3.76 3.75 3.73 3.64 3.63 3.63 3.63 3.62 3.62 3.62 3.62 3.62
cisbp_M4010 istpar_M40108.2 factorbook_TBP taipale_NR3C2_DBD_NRGNACANNITGTINCYN dbcorrdb_FOXA1_ENCSR000BPX_1_m1 homer_CTATAAAAGCSV_TATA-box cisbp_M6367 elemento_GGCGCC transfac_pro_M02263 dbcorrdb_GTT2F1_ENCSR000EHC_1_m1 cisbp_M5460 transfac_pro_M02240 stark_STATAWAYSVVV neph_UV_MotIf0510 swisregulon_pk_FOX3.92 hdpl_ERM35A tidimers_M00384 neph_UV_MotIf0241 transfac_pro_M0383	TBP (directAnnotation). POLR2A; TAF1; TBP (directAnnotation). NR3C2 (directAnnotation). FOXA1 (directAnnotation). FOXA1 (directAnnotation). NFE2L2 (directAnnotation). GTF2F1 (directAnnotation). GTF2F1 (directAnnotation). GTF2F1 (directAnnotation). TFP; TBP12 (directAnnotation). TEXP3 (directAnnotation). EXPP3 (directAnnotation). EXPP3 (directAnnotation). EXPP3 (directAnnotation). EXPP3 (directAnnotation). EXP1 (directAnnotation). EXP1 (directAnnotation). EXP2 (directAnnotation). EXP3 (direct	Gir24; 6:172; FOURAC, 142; Interredely_MotifSmilarity), 18/22 (interredey_MotifSmilarity, D-thology), GT28; 6:172; FJ2F; FV0R2A; T42; 138* (interredely_MotifSmilarity), T8PL2 (interredey_MotifSmilarity, D-thology), GT28; 6:172; FJ2F; NELFE (interredey_MotifSmilarity), T8PL2 (interredey_MotifSmilarity, D-thology), AR; FOXA; NR3C; (interredey_MotifSmilarity), FS1; HS2; HS54 (interredey_MotifSmilarity, D-thology), AR; RIXA; NR3C; FORE [interredey_MotifSmilarity], HS1; HS2; HS54 (interredey_MotifSmilarity, D-thology), AR; RIXA; T43; T88 (interredey_MotifSmilarity), T8PL2 (interredey_MotifSmilarity, D-thology), BAC+1; IACH2; FOS; FOSE; FOS1; FOS1; FOS2; JUN; UNR; UNR; UNR; UNR; MAFE; M	3.82 3.83 3.78 3.77 3.76 3.77 3.76 3.77 3.76 3.77 3.77
cisbp_M4010 isspar_M40108.2 factorbook_TBP taipale_NR3C2_DBD_NRGNACANNITGTNCYN dbcorrdb_FOXA1_ENCS0000BPX_1_m1 homer_CTATAAAAGCSV_TATA-box cisbp_M56367 elemento_GGGGGCC transfac_pro_M02263 dbcorrdb_GTF2F1_ENCSR000EHC_1_m1 cisbp_M5460 transfac_pro_M01240 stark_STATAWAWISVV neph_UW_NctifoS10 swiszegulon_tx_FCXF3.92 hdpl_BRM53A ttdimer_M000384 neph_UW_Nctifo241	TBP (directAnnotation). POLR2A, TAF1; TBP (directAnnotation). NR3C2 (directAnnotation). FOXA1 (directAnnotation). NFE212 (directAnnotation). GTF2F1 (directAnnotation). GTF2F1 (directAnnotation). GTF2F1 (directAnnotation). FOXL1 (directAnnotation). FOXL1 (directAnnotation). FOXL1 (directAnnotation). GTF2F1RD1 (directAnnotation). IBP; IBP12 (netronation). IBP; IBP12 (netronation). IBP2F1 (directAnnotation). IBP2F1 (directAnnotation). IBP2F1 (directAnnotation). IBP3F1 (directAnnotation). IBP3F1 (directAnnotation). IBP3F1 (directAnnotation). IBP3F1 (directAnnotation). IBP3F1 (directAnnotation). IBF3F1 (directAnnotation).	Gir2di, Gir2di, POLKAA, KP3, Interredely, MottiSminiarity), IBPL2 (inferredely, MottiSminiarity, DFNL2 (inferredely, Mott	3.82 3.83 3.78 3.77 3.77 3.76 3.75 3.73 3.64 3.63 3.64 3.63 3.64 3.63 3.64 3.65 3.65 3.65 3.65 3.65 3.65 3.65 3.65
cisbp_M4010 isopar_M40108.2 factorbook_TBP taipale_NR3C2_DBD_NRGNACANNITGTINCYN dbcorrdb_FOXA1_ENCSR000BPX_1_m1 homer_CTATAAAAGCSV_TATA-box cisbp_M6367 elemento_GCGCCCC transfac_pro_M02263 dbcorrdb_GTF2F1_ENCSR000EHC_1_m1 cisbp_M5460 transfac_pro_M02263 dbcorrdb_GTF2F1_ENCSR000EHC_1_m1 cisbp_M5460 transfac_pro_M02263 dbcorrdb_GTF2F1_ENCSR000EHC_1_m1 cisbp_M5460 transfac_pro_M02263 dbcorrdb_GTF2F1_ENCSR000EHC_1_m1 cisbp_M5460 transfac_pro_M02263 transfac_pro_M0240 tark_STATAWAWRSVV neph_LVV.MotifC310 startsfac_M00384 neph_LVV.MotifC241 transfac_pro_M02843 ispgr_M0588.1 transfac_pro_M02815	TBP (directAnnotation). POLR2A; TAF1; TBP (directAnnotation). NR3C2 (directAnnotation). FOXA1 (directAnnotation). FOXA1 (directAnnotation). NFE2 (directAnnotation). GTF2F1 (directAnnotation). GTF2F1 (directAnnotation). GTF2F1 (directAnnotation). FOXL1 (directAnnotation). FOXL1 (directAnnotation). EXPP (directAnnotation). EXP (directAnnota	G1728; G1721; D1721; P0UKAC, IV31; Interredely_MottISmiliarity), IBP12 G1728; G1721; D1721; D1721; D1741; D1740; D0740; D0740; D1741; D1721;	3.82 3.83 3.77 3.77 3.76 3.75 3.73 3.64 3.63 3.62 3.62 3.62 3.62 3.62 3.59 3.59 3.59 3.59 3.59 3.59 3.53 3.53
cisbp_M4010 isspar_M40108.2 factorbook_TBP taipale_NR3C2_D8D_NRGNACANNITGTNCYN dbcorrdb_FOXA1_ENCSR000BPX_1_m1 homer_CTATAAAAGCSV_TATA-box cisbp_M56367 elemento_GGGGGCC transfac_pro_M02263 dbcorrdb_GTF2F1_ENCSR000EHC_1_m1 cisbp_M5460 transfac_pro_M01240 stark_STATAWAWISSVV neph_UW_NctifC510 swisregulon_thc_FCXF3.02 hdp1_BRM55A ttdimer_M000384 neph_UW_NctifC411 transfac_pro_M0383 ttdimer_m00384.1 transfac_pro_M029515 transfac_m0_M029515 transfac_m0_M00516	TBP (directAnnotation). POLR2A, TAF1; TBP (directAnnotation). NR3C2 (directAnnotation). FOXA1 (directAnnotation). NFE2 (directAnnotation). NFE212 (directAnnotation). GTF2F1 (directAnnotation). GTF2F1 (directAnnotation). GTF2F1 (directAnnotation). FOXL1 (directAnnotation). GTF2RD1 (directAnnotation). SFDEP1 (directAnnotation). UR72; STAT1 (directAnnotation). UR72; STAT1 (directAnnotation). SFDEF1	Gir2di, Gir2di, POLKAA, IAB L (Interedelly_MottiSimilarity), IBPL2 (interedely_MottiSimilarity, D-THOLOGy), GTF28, GTF28, FDF28, TAF21, IBP (interedelly_MottiSimilarity), TBPL2 (interedely_MottiSimilarity, D-Thology), GTF28, GTF28, INTERE (interedely_MottiSimilarity), TBPL2 (interedely_MottiSimilarity, D-Thology), AR, FOXAL, INR3C, (interedely_MottiSimilarity), TBPL2 (interedely_MottiSimilarity, D-Thology), AR, INR3C,	3.82 3.83 3.78 3.77 3.77 3.76 3.77 3.76 3.73 3.64 3.63 3.64 3.63 3.62 3.62 3.62 3.62 3.62 3.62 3.62
cisbp_M4010 jspar_M40108.2 factorbook_TBP taipale_NR3C2_DBD_NRGNACANNITGTINCYN dbcorrdb_FOXA1_ENCSR000BPX_1_m1 homer_CTATAAAAGCSV_TATA-box cisbp_M6367 elemento_GCGCCCC transfac_pro_M02263 dbcorrdb_GTF2F1_ENCSR000EHC_1_m1 cisbp_M5460 transfac_pro_M02263 dbcorrdb_GTF2F1_ENCSR00EHC_1_m1 cisbp_M5460 transfac_pro_M02263 dbcorrdb_GTF2F1_ENCSR00EHC_1_m1 cisbp_M5460 transfac_Pro_M0284 transfac_Pro_M0284 transfac_PC_M0284 transfac_PC_M0284 transfac_PC_M2835 transfac_PC_M285 transfac_PC_M285 tra	TBP (directAnnotation). POLR2A; TAF1; TBP (directAnnotation). NR3C2 (directAnnotation). FOXA1 (directAnnotation). FOXA1 (directAnnotation). NFE2 (directAnnotation). GTF2F1 (directAnnotation). GTF2F1 (directAnnotation). GTF2F1 (directAnnotation). FOXL1	Gir24; 6:17-21; PULKAC, IV3 Linterredely_MottISimiliarity), IBPL2 (inferredely_MottISimiliarity, DFR2, MottISimiliarity), TBPL2 (inferredely_MottISimiliarity, DFR2, MottISimiliarity, TBPL2 (inferredely_MottISimiliarity, DFR2, MottISimiliarity, TBPL2 (inferredely_MottISimiliarity, DFR2, MottISimiliarity, TBPL2 (inferredely_MottISimiliarity, DFR2, MottISimiliarity, DFR2, MOTA, FRANCE,	3.82 3.83 3.78 3.77 3.77 3.76 3.75 3.73 3.66 3.63 3.64 3.63 3.64 3.63 3.62 3.62 3.62 3.62 3.62 3.55 3.55 3.55 3.55 3.55 3.55 3.55 3.5
cisbp_M4010 isspar_M40108.2 factorbook_TBP taipale_NR3C2_DBD_NRGNACANNITGTNCYN dbcorrdb_FOXA1_ENCSR000BPX_1_m1 homer_CTATAAAAGCSV_TATA-box cisbp_M56367 elemento_GCGGCGC transfac_pro_M02263 dbcorrdb_GTF2F1_ENCSR000EHC_1_m1 cisbp_M5460 transfac_pro_M01240 stark_STATAWAWRSVVV neph_UW_NdtYOV stark_STATAWAWRSVVV neph_UW_NdtYO41 transfac_pro_M0384 neph_UW_NdtYO41 transfac_pro_M0383 may method transfac_pro_M0383 transfac_pro_M0384 transfac_pro_M0384 transfac_pro_M0384 transfac_pro_M0384 transfac_pro_M0384 transfac_pro_M0384 transfac_pro_M0383 paper_M03684.1 transfac_pro_M0384 t	TBP (directAnnotation). POLR2A; TAF1; TBP (directAnnotation). NR3C2 (directAnnotation). FOXA1 (directAnnotation). NFE2 (directAnnotation). NFE212 (directAnnotation). GTF2F1 (directAnnotation). GTF2F1 (directAnnotation). GTF2RD1 (directAnnotation). TBP, TBP12 (InferredBy_Orthology). POXP3 (directAnnotation). IXEF2; STAT1 (directAnnotation). IXEF2; STAT1 (directAnnotation). SPDEF (inferredBy_Orthology). PPARGCIA (directAnnotation).	Girzdis, Dirzzi, POLKAZ, KP3, Interredely, MottiSmiliarity), IBPL2 (interredely, MottiSmiliarity, D_THOLGQ), GTF28, CTF21, DECRAZ, KF21, TBP (inferredely, MottiSmiliarity), TBPL2 (inferredely, MottiSmiliarity, D_THOLGQ), GTF28, CTF21, NELFE (inferredely, MottiSmiliarity), TBPL2 (inferredely, MottiSmiliarity, D_THOLGQ), AR, FOXAL, INR3C, (inferredely, MottiSmiliarity), TBPL2 (inferredely, MottiSmiliarity, D_THOLGQ), AR, ROXAL, INR3C, (inferredely, MottiSmiliarity), TBPL2 (inferredely, MottiSmiliarity, D_THOLGQ), AR, ROXAL, NR3C, (inferredely, MottiSmiliarity), TBPL2 (inferredely, MottiSmiliarity, D_THOLGQ), AR, ROXAL, FOXAL, FOX, D_COX2, UNX, UNB, UND, MAF; MAFB; MAFF; MAFG; MAFC, NFE2L1, NR3C, FOX, FOXAL, TOXAL, MOTTISmiliarity), DLR2A, TAF1, TBP (inferredely, MottiSmiliarity), CTF28, IRLEF; POLR2A, TAF1, TBP (inferredely, MottiSmiliarity), GTF28, IRLEF; POLR2A, TAF1, TBP (inferredely, MottiSmiliarity), CTF28, IRLEF; POLR2A, TAF1, TBP (inferredely, MottiSmiliarity), GTF28, IRLEF; POLR2A, TAF1, TBP (inferredely, MottiSmiliarity), CTF28, IRLEF; POLR2A, TAF1, TBP (inferredely, MottiSmiliarity), POLR2A, TAF1 (inferredBy, MottiSmiliarity), POLR2A, TAF1 (inferredBy, MottiSmiliarity), MEF24, IMEF2C (inferredBy, MottiSmiliarity),	3.82 3.83 3.78 3.77 3.77 3.76 3.75 3.73 3.64 3.63 3.62 3.62 3.62 3.62 3.55 3.55 3.55 3.55 3.54 3.53 3.51 3.51 3.51
cisbp_M4010 isipar_M40108.2 factorbook_TBP taipale_NR3C2_DBD_NRGNACANNITGTINC'N dbcorrdb_FOXA1_ENCSR000BPX_1_m1 homer_CTATAAAAGCSV_TATA-box cisbp_M6367 elemento_SCGCGCC transfac_pro_M02263 dbcorrdb_GTF2F1_ENCSR000EHC_1_m1 cisbp_M5460 transfac_pro_M02263 dbcorrdb_GTF2F1_ENCSR000EHC_1_m1 cisbp_M5460 transfac_pro_M02263 dbcorrdb_GTF2F1_ENCSR000EHC_1_m1 cisbp_M5460 transfac_pro_M02263 dbcorrdb_GTF2F1_ENCSR000EHC_1_m1 cisbp_M5460 transfac_pro_M02263 transfac_pro_M02363 transfac_pro_M02384 neph_UVM_M01f0214 transfac_pro_M02383 japar_M0548.1 transfac_pro_M0248 transfac_pro_M0	TBP (directAnnotation). POLR2A; TAF1; TBP (directAnnotation). NR3C2 (directAnnotation). FOXA1 (directAnnotation). NFE2 (directAnnotation). NFE2 (directAnnotation). GTF2F1 (directAnnotation). GTF2F1 (directAnnotation). GTF2F1 (directAnnotation). FOXL1 (directAnnotation). FOXL1 (directAnnotation). SFDEF (inferredBy_Orthology). PARGC1A (directAnnotation).	Gir24; 6:1721; POLKAC, IV21; Intercedely_MotifSimilarity), IBP12 (inferredely_MotifSimilarity, DFN2 Gir26; 6:1721; POLKA2, TA21; IBP (inferredely_MotifSimilarity), TBP12 (inferredely_MotifSimilarity, DFN2 Gir26; 6:1721; NELFE (inferredely_MotifSimilarity), TBP12 (inferredely_MotifSimilarity, DFN2 (inferredely_MotifSimilarity), DFN2 (inferredely_MotifSimilarity), TBP12 (inferredely_MotifSimilarity), TBP12 (inferredely_MotifSimilarity), TBP12 (inferredely_MotifSimilarity), TBP12 (inferredely_MotifSimilarity), TBP13; HSF2; HSF4 (inferredely_MotifSimilarity), TBP12 (inferredely_MotifSimilarity), TDD12; FOX3; FOX01; FOX3; FOX01; FOX1; FOX01; FOX2; FOX01; FOX1; FOX01; FOX2; FOX01; FOX1; FOX01; FOX2; FOX01; FOX1; FOX01; FOX01; FOX01; FOX1; FOX01; FOX01; FOX01; FOX1; FOX01; FOX1; FOX01; FOX01; FOX01; FOX1; FOX01; F	3.82 3.8 3.77 3.77 3.77 3.76 3.75 3.64 3.64 3.64 3.64 3.64 3.64 3.64 3.64
cisbp_M4010 isspar_M40108.2 factorbook_TBP taipale_NR3C2_DBD_NRGNACANNINTGTNCYN dbcorrdb_FOXA1_ENCSR000BPX_1_m1 home_CTATAAAAGCSV_TATA-box cisbp_M6367 elemento_GCGCGCC transfac_pro_M02263 dbcorrdb_GTF2F1_ENCSR000EHC_1_m1 cisbp_M5460 transfac_pro_M01240 stark_STATAWAWRSVVV neph_UW_MctiOS10 swisregulon_hx_FOXF3.2 hdj_IBM35A tfdimer_M000384 neph_UW_MctiO241 transfac_pro_M0383 japar_M0358.1 transfac_pro_M0383 ispar_M0358.1 transfac_pro_M0383 ispar_M0358.1 transfac_pro_M0384 transfac_pro_M0383 ispar_M0358.1 transfac_pro_M0383 ispar_M0358.1 transfac_pro_M0383 ispar_M0358.1 transfac_pro_M0384 transfac_pro_M0383 ispar_M0358.1 transfac_pro_M0384 transfac_pro_M0384 ispar_M0358.1 transfac_pro_M0385 ispar_M0358.1 transfac_pro_M0385 ispar_M0358.1 transfac_pro_M0385 ispar_M0358.1 transfac_pro_M0385 ispar_M0358.1 transfac_pro_M0385 ispar_M0358.1 transfac_pro_M0385 ispar_M0358.1 transfac_pro_M0385 ispar_M0358.1 transfac_pro_M0385 ispar_M0358.1 transfac_pro_M0385 ispar_M0358.1 transfac_pro_M0385 ispar_M0358.1 transfac_pro_M0385 ispar_M0358.1 transfac_pro_M0385 ispar_M0358.1 transfac_pro_M0385 ispar_M0358.1 transfac_pro_M0385 ispar_M0358.1 transfac_pro_M0385 ispar_M0358.1 transfac_pro_M0385 ispar_M0358 ispar_	TBP (directAnnotation). POLR2A; TAF1; TBP (directAnnotation). NR3C2 (directAnnotation). NF22 (directAnnotation). NF22 (directAnnotation). NF22 (directAnnotation). GTF2F1 (directAnnotation). GTF2F1 (directAnnotation). GTF2F1 (directAnnotation). GTF2RD1 (directAnnotation). SPDEF (inferendBy_Orthology). PPARGC1A (directAnnotation).	Girzdis, Dirzhi, POUKAA, IVA Linterredely, MottiSmiliarity), IBPL2 (inferredely, MottiSmiliarity, D_FNL2 (inferredely, MottiSmiliarity), DEVL2 (i	3.82 3.8 3.78 3.77 3.76 3.77 3.76 3.73 3.64 3.63 3.64 3.63 3.62 3.62 3.62 3.62 3.55 3.55 3.55 3.55 3.53 3.51 3.51
cisbp_M4010 jsipar_M40108.2 factorbook_TBP taipale_NR3C2_DBD_NRGNACANNITGTINCYN dbcorrdb_FOXA1_ENCSR000BPX_1_m1 homer_CTATAAAAGCSV_TATA-box cisbp_M5367 elemento_GCGCCGC transfac_pro_M02263 dbcorrdb_GTF2F1_ENCSR000EHC_1_m1 cisbp_M5460 transfac_pro_M01240 stark_STATAWAWRSVW neph_UW_MetH0510 awitsregulon_hs_FOXF3.p2 hdpl_m8058A ttimers_M00384 neph_UW_MetH0510 perform_M0588.1 ttransfac_pro_M02363 jspar_M0588.1 ttransfac_pro_M02363 preferem_nrMoS81.1 ttransfac_pro_M02363 theorem to the transfac_m0383 the transfac_m038 the tr	TBP (directAnnotation). POLR2A; TAF1; TBP (directAnnotation). NR3C2 (directAnnotation). FOXA1 (directAnnotation). NFE2 (directAnnotation). NFE2 (directAnnotation). GTF2F1 (directAnnotation). GTF2F1 (directAnnotation). GTF2F1 (directAnnotation). FOXL1 (directAnnotation). SFDEF (inferredBy_Orthology). PARGC1A (directAnnotation). SFDEF (inferredBy_Orthology). FOXB (directAnnotatio	Girzés (J. 121); POURA, IVA 1, Interredely_MotifSimilarity), IBP12 (inferredely_MotifSimilarity, D-Thology), GTP28; GTP21; DF21; BT21; BT2 (inferredely_MotifSimilarity), TBP12 (inferredely_MotifSimilarity, D-Thology), GTP28; GTP21; DF21; DF21; DF21; DF21; DF21; DF21; DF22; DF21; DF22; DF21; DF21; DF21; DF22; DF22; DF21; DF21; DF22; DF21; DF22; DF21; DF21; DF22; DF21; DF22; DF21; DF21; DF22; DF21; DF21; DF22; DF21; DF21; DF22; DF21; DF22; DF21; DF21; DF22; DF21; DF21; DF22; DF21; DF22; DF21; DF21; DF22; DF21; DF21; DF22; DF21; DF21; DF22; D	3.82 3.8 3.77 3.77 3.77 3.76 3.75 3.64 3.63 3.64 3.63 3.64 3.63 3.64 3.62 3.62 3.62 3.62 3.62 3.55 3.55 3.55 3.55 3.55 3.55 3.55 3.5
cisbp_M4010 isspar_M40108.2 factorbook_TBP taipale_NI3C2_DBD_NRGNACANNINTGTNCYN dbcorrdb_FOXA1_ENCSR000BPX_1_m1 homer_CTATAAAAGCSV_TATA-box cisbp_M6367 elemento_GCGCGCC transfac_pro_M02263 dbcorrdb_GT72F1_ENCSR000BHC_1_m1 cisbp_MS460 transfac_pro_M01240 stark_STATAWAWRSVVV neph_UW_Mctif0510 swisregulon_hs_FOX73.p2 hdpi_ERM53A ttdimer_M000384 neph_UW_Mctif041 transfac_pro_M0383 japar_M40584.1 ttransfac_pro_M0383 japar_M0584.1 ttransfac_pro_M0384 japar_M0584.1 ttransfac_pro_M0383 japar_M0584.1 ttransfac_pro_M0384 japar_M0584.1 ttransfac_pro_M0398 japar_M0584 japar_M058 j	TBP (directAnnotation). POLR2A; TAF1; TBP (directAnnotation). NR3C2 (directAnnotation). NR3C2 (directAnnotation). NFE2 (directAnnotation). NFE2 (directAnnotation). GTF2F1 (directAnnotation). GTF2F1 (directAnnotation). GTF2F1 (directAnnotation). SPDEF (inferredBy_Orthology). POKP3 (directAnnotation). KE72; STAT1 (directAnnotation). KE72; STAT1 (directAnnotation). FOXL1 (directAnnotation).	Girzdis, Dirzzi, POUKAC, Nat J. Interredby, MottiSmillarity), IBPL2 (inferredby, MottiSmillarity, D, Chrology), GTP28, CTP21, POUR2A, TA73, TBP (inferredby, MottiSmillarity), TBPL2 (inferredby, MottiSmillarity, D, Chrology), GTP28, CTP21, NELFE (inferredby, MottiSmillarity), TBPL2 (inferredby, MottiSmillarity, D, Chrology), AR, FOXAL, NR3C1, (inferredby, MottiSmillarity), TBPL2 (inferredby, MottiSmillarity, D, Chrology), AR, ROXAL, TA73, TBP (inferredby, MottiSmillarity), TBPL2 (inferredby, MottiSmillarity, D, Chrology), AR, ROXAL, TA73, TBP (inferredby, MottiSmillarity), TBPL2 (inferredby, MottiSmillarity, D, Chrology), BAC(1); BAC(1); FOS, FOS1, FOS2, I, FOS2, I, M, JUNB; JUND; MAF; MAFB; MAFF; MAFG; MAFR; NFE2L1, NFE2L; MFE12 (inferredby, MottiSmillarity), EAC(1); BAC(1); EAC(1); FOS, FOS1, FOS2, I; FOS2, I, FOS2, FOS2, FOS4, I, FOS2, FOS2, FOS4, I, FOS2, F	3.82 3.8 3.77 3.77 3.76 3.73 3.76 3.64 3.63 3.63 3.63 3.64 3.63 3.63 3.6
cisbp_M4010 jspar_M40108.2 factorbook_TBP taipale_NR3C2_DBD_NRGNACANNITGTINCYN dbcorrdb_FOXA1_ENCSR000BPX_1_m1 homer_CTATAAAAGCSV_TATA-box cisbp_M54367 elemento_GCGCGCC transfac_pro_M02263 dbcorrdb_GTF2F1_ENCSR000EHC_1_m1 cisbp_M5460 transfac_pro_M01240 stark_STATAWAWR5VW neph_UVM_buit/0510 switurspion_hs_FCXP3.p2 hdpi_RBM35A titiomer_M00384 titipale_FCXL1_FULENCSR000EEQ.1_m1	TBP (directAnnotation). POLR2A; TAF1; TBP (directAnnotation). NR3C2 (directAnnotation). FOXA1 (directAnnotation). NFE2 (directAnnotation). NFE212 (directAnnotation). GTF2F1 (directAnnotation). GTF2F1 (directAnnotation). GTF2F1 (directAnnotation). FOXL1 (directAnnotation). SPDEF (inferredBy_Orthology). PPABGC1A (directAnnotation). FOXL1 (directAnnotation). SPDEF (inferredBy_Orthology). SPDEF (infe	Girzés (J. 121): POLKAZ, IVA 1. Interredely_MotifSimilarity), IBPL2 (inferredely_MotifSimilarity, D-Thology), GTP28, CTF21; DF21; DF1(efferedely_MotifSimilarity), TBPL2 (inferredely_MotifSimilarity, D-Thology), GTP28, CTF21; NELFE (inferredely_MotifSimilarity), TBPL2 (inferredely_MotifSimilarity, D-Thology), AR, RGXX1, NR3C1 (inferredely_MotifSimilarity), TBPL2 (inferredely_MotifSimilarity, D-Thology), AR, RGXX1, NR3C1 (inferredely_MotifSimilarity), TBPL2 (inferredely_MotifSimilarity, D-Thology), AR, RGXX1, RGX2, PGR (inferredely_MotifSimilarity), TBPL2 (inferredely_MotifSimilarity, D-Thology), BCX1; RGX1; FDS1; PGR (inferredely_MotifSimilarity), TBPL2 (inferredely_MotifSimilarity, D-Thology), BCX1; RGX1; FDS1; FDS1; FDS1; FDS1; FDS1; FDS2; IVNL UNB; UND; MAF; MAF; MAF; MAF; MAF; MAF; MAF; MAF	3.82 3.8 3.77 3.77 3.77 3.76 3.73 3.64 3.63 3.64 3.62 3.62 3.62 3.62 3.62 3.62 3.62 3.55 3.55 3.55 3.51 3.51 3.51 3.51 3.55 3.55
cisbp_M4010 isspar_M40108.2 factorbook_TBP taipale_NI3C2_DBD_NRGNACANINITGTNCYN dbcorrdb_FOXA1_ENCSR000BPX_1_m1 homer_CTATAAAAGCSV_TATA-box cisbp_M6367 elemento_GCGCGCC transfac_pro_M02263 dbcorrdb_GTF2F1_ENCSR000EHC_1_m1 cisbp_M5460 transfac_pro_M01240 stark_STAXWAWRSVV neph_UVM.bdfG510 switergolon_th_FCX7.9.2 hdpl_R8M35A ttdimer_M000384 neph_UVM.bdfG210 switerG010 switerG010 stark_STAXWAWRSVV rearder_m1M00384 neph_UVM.bdfG210 transfac_pro_M0383 japar_M00584.1 ttransfac_pro_M0383 japar_M00584.1 ttransfac_pro_M0383 japar_M00584.1 ttransfac_pro_M0383 japar_M00584.1 ttransfac_pro_M0383 japar_M00584.1 ttransfac_pro_M0383 japar_M00584.1 ttransfac_pro_M0383 japar_M00584.1 ttransfac_pro_M0384.1 ttransfac_pro_M0384.1 ttransfac_pro_M0384.1 ttransfac_pro_M0385 japar_M00584.1 ttransfac_N0580 japar_M00584 japar_M00588 jap	TBP (directAnnotation). POLR2A; TAF1; TBP (directAnnotation). NR3C2 (directAnnotation). R3C2 (directAnnotation). NFE2 (directAnnotation). NFE2 (directAnnotation). SF2E1 (directAnnotation). GTF2F1 (directAnnotation). GTF2F1 (directAnnotation). SF2F3 (directAnnotation). SF2F3 (directAnnotation). SF2F3 (directAnnotation). SF2F1 (di	Girzés (J. 121); POURA, IAP L Interredby MottSimilarity), IBPL2 (inferredby, MottSimilarity, D. PUL2 (inferredby, MottSimilarity), D. PUL2 (inferredby, MottSimilarity, D. PUL2 (inferredby, MottSimilarity), D. PUL2 (inferr	3.82 3.8 3.77 3.76 3.77 3.76 3.73 3.64 3.63 3.63 3.63 3.63 3.63 3.63 3.6
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 Table S9: Cerebellar Bergmann Glia output from RCisTarget for premutation vs. control comparison. Continued on next page.
 3.45

		EQXA1 - EQXA2 - EQXA3 - EQXC1 - EQXC2 - EQXD3 - EQXE1 - EQXE1 - EQXE1 - EQXI1 - EQXI1 - EQXI1 - EQXI2	
		FOXIA; FO	
- here are		(inferredBy_MotifSimilarity). FOXB1; FOXN2; FOXN3; FOXO3; FOXO3; FOXP4	2.45
cisbp_M5446	FOXD2 (directAnnotation).	(interredBy_Motifsimilarity_n_Orthology).	3.45
		FOXO1; FOXO4; FOXO6; FOXP1 (inferredBy_MotifSimilarity). FOXD1; FOXD4; FOXD4; FOXD4L1;	
	FORMAR S. Construction of the Internal	FOXD4L3; FOXD4L4; FOXD4L5; FOXD4L6; FOXJ3; FOXN2; FOXN3; FOXO3; FOXP2; FOXP3; FOXP4	
transfac_pro_M05297	SOX1 (directAnnotation).	SOX3 (inferredBy_MotifSimilarity_n_Orthology).	3.44
transfac_pro_M09232		HSF1; HSF2 (inferredBy_MotifSimilarity).	3.44
		FOXC1; FOXC2; FOXD2; FOXD3; FOXF1; FOXF2; FOXG1; FOXI1; FOXJ1; FOXJ2; FOXL1; FOXL2;	
		FOXO1; FOXO4; FOXO6; FOXP1; FOXP3 (inferredBy_MotifSimilarity). FOXD1; FOXD4; FOXD4L1; FOXD4L2; FOXD4L4; FOXD4L5; FOXD4L6; FOXD2; FOXD2; FOXD2; FOXD2; FOXD4; FOXD4L1;	
cisbp_M6019	FOXK1 (inferredBy_Orthology).	(inferredBy_MotifSimilarity_n_Orthology).	3.43
cisbp_M3450	IKZF1 (directAnnotation).		3.42
cisbp_M5985	AR (inferredBy_Orthology).	NR3C1; NR3C2 (inferredBy_MotifSimilarity). BACH1- BACH2- EOS- EOSE EOSE 1- EOSE 2- ILIN- ILINE- ILINE- MAEE- MAEG- MAEK- NEE2	3.42
swissregulon_hs_NFE2L2.p2	NFE2L2 (directAnnotation).	(inferredBy_MotifSimilarity). ATF3 (inferredBy_MotifSimilarity_n_Orthology).	3.41
		FOXA1; FOXA2; FOXB1; FOXC1; FOXC2; FOXD1; FOXD2; FOXG1; FOXI1; FOXJ2; FOXJ3; FOXK1;	
		FOXL1; FOXO1; FOXO3; FOXO4; FOXO6; FOXQ1 (inferredBy_MotifSimilarity). FOXD3; FOXD4; FOXD4I 1: FOXD4I 3: FOXD4I 4: FOXD4I 5: FOXD4I 6: FOXF1: FOXF2: FOXD2: FOXD3: SRF	
cisbpM0750	FOXP1; FOXP2; FOXP3; FOXP4 (inferredBy_Orthology).	(inferredBy_MotifSimilarity_n_Orthology).	3.41
swissregulon_sacCer_YDR520C			3.4
cisbp M4681	BACH1 (directAnnotation).	BACH2; JUN; MAF; MAFA; MAFB; MAFF; MAFG; MAFK; NFE2; NFE2L1; NFE2L2; NFE2L3 (inferredBy MotifSimilarity).	3.4
		FOXC2; FOXD2; FOXD3; FOXF1; FOXF2; FOXG1; FOXI1; FOXJ1; FOXJ3; FOXK1; FOXL1; FOXO1;	
		FOXO3; FOXO4; FOXP1; FOXP2; FOXP3; FOXQ1 (inferredBy_MotifSimilarity). FOXD1; FOXD4;	
taipale FOXJ2 DBD RTAAACAA	FOXJ2 (directAnnotation).	FOXD4L1; FOXD4L3; FOXD4L4; FOXD4L5; FOXD4L6; FOXI2; FOXI2; FOXK2; FOXL2; FOXN2; FOXN3; FOXO6; FOXP4 (inferredBy MotifSimilarity n Orthology).	3.39
predrem_nrMotif334			3.39
		AR; FOXA1; PGR (inferredBy_MotifSimilarity). HSF1; HSF2; HSF4	2.20
transfac_proM09240	maca (un debutitotation).	HSF1 (inferredBy_MotifSimilarity).	3.38
cisbpM2341		MEF2A; MEF2C (inferredBy_MotifSimilarity).	3.36
cisbp_M2288 taipale cut meth H0XA13 NCCAATAAAAA oDBD room	HSF1 (directAnnotation).	HOXB2; HSF2; HSF4 (inferredBy_MotifSimilarity).	3.36
elemento_CGAGCGC	noves preciamination).	nonozo, nonezo, nonozo (mereuby_worrormilanty).	3.35
swissregulon_hs_HSF1_2.p2	HSF1; HSF2 (directAnnotation).	HSF4 (inferredBy_MotifSimilarity_n_Orthology).	3.35
homer NAGAACAGNCTGTTCT GRE		AR; FOXA1; NR3C1; NR3C2; PGR (inferredBy_MotifSimilarity). HSF1; HSF2; HSF4 (inferredBy_MotifSimilarity_n_Orthology)	2.22
taipale_Ar_DBD_RRGNACANNNTGTNCYY_repr	AR (inferredBy_Orthology).	NR3C1; NR3C2 (inferredBy_MotifSimilarity).	3.33
elemento_CGCGCGC			3.3
		FOXC2; FOXD2; FOXD3; FOXF1; FOXF2; FOXG1; FOXI1; FOXJ1; FOXJ3; FOXK1; FOXL1; FOXN2;	
		FUXU1; FUXU3; FOXO4; FOXP1; FOXP2; FOXP3; FOXQ1 (inferredBy_MotifSimilarity). FOXA2; FOXD1; FOXD4; FOXD4L1; FOXD4L3; FOXD4L4; FOXD4L5: FOXD4L6: FOX12: FOX13: FOXL2:	
cisbpM5454	FOXJ2 (directAnnotation).	FOXL2; FOXN3; FOXO6; FOXP4 (inferredBy_MotifSimilarity_n_Orthology).	3.29
		BACH1; EP300; FOS; FOSB; FOSL1; FOSL2; JUN; JUNB; JUND; MAF; MAFB; MAFF; MAFG; MAFK;	
hocomoco BACH2 HUMAN.H11MO.0.A	BACH2 (directAnnotation).	NFE2; NFE2L1; NFE2L2; NFE2L3; NRF1 (inferredBy_MotifSimilarity). ATF3 (inferredBy_MotifSimilarity_n_Orthology).	3.27
transfac_pro_M07568		HSF1; HSF2; HSF4 (inferredBy_MotifSimilarity).	3.27
transfac_proM01128			3.27
taipale_tf_pairsHOXB2_ESRRB_TAATKRNNNNNAAGGTCA_CAP_repr	ESRRB; HOXB2 (directAnnotation).	GTE28- POL R2A-TAE1-TRP (inferredBy: MotifSimilarity) TRPI 2	3.26
dbcorrdb_GTF2F1_ENCSR000EBP_1_m1	GTF2F1 (directAnnotation).	(inferredBy_MotifSimilarity_n_Orthology).	3.26
tfdimers_MD00429	ARID3A; IKZF2 (directAnnotation).		3.24
tfdimers_MD00082	GATA1; GATA2; GATA3; GATA4; GATA5; GATA5; ZNF217 (directAnnotation).		3.23
tainale tf nairs HOXB2 SOX15 ACAAWRSNNNNYMATTA CAP repr	HOXB2: SOX15 (directAnnotation).		3.23
taipale_tf_pairs_HOX82_SOX15_ACAAWRSNNNNYMATTA_CAP_repr factorbook_HSF1	HOXB2; SOX15 (directAnnotation). HSF1 (directAnnotation).	HOXB2; HSF2; HSF4 (inferredBy_MotifSimilarity).	3.23
taipale_tf_pairs_HOXB2_SOX15_ACAAWRSNNNNYMATTA_CAP_repr factorbook_HSF1 cisbp_M2351	HOXB2; SOX15 (directAnnotation). HSF1 (directAnnotation).	HOX82; HSF2; HSF4 (inferredBy_MotifSimilarity). MEF2A; MEF2C (inferredBy_MotifSimilarity).	3.23 3.19 3.19
tapaje tr pains_HOX82_SOX15_ACAAWRSNNNYMATTA_CAP_repr factorbook_HSF1 cisbp_M2351 hacomoco_ANDR_MOUSE H11M0.0.A	HOX82; SOX15 (directAnnotation). HSF1 (directAnnotation). A8 (inferredBy Ortholosy).	HOKB2; HSF2; HSF4 (inferredBy_MotifSimilarity). MEF2A; MEF2C (inferredBy_MotifSimilarity). FOXA1; NRS11; NRS12; NRS(inferredBy_MotifSimilarity). HSF1; HSF2; HSF4 (inferredBy_MotifSimilarity, n_CHIstope).	3.23 3.19 3.19 3.19
tapide_T_pais_HOR2_SOI15_ACAAWESNNNYMATA_CAP_repr factorbook_HP3 citbg_M2531 hocomoco_JANR_MOUSE H11MO.0.0 tapide_AR_BOB_RROWACANINTCTWCY	HXX82; SDX15 (directAnnotation). HSF1 (directAnnotation). AR (inferredBy_Orthology). AR (directAnnotation).	HOK82; HSF2; HSF4 (inferredBy_MotIfSimilarity). MEF2A; MEF2C (inferredBy_MotIfSimilarity). FOXA1; M88C1; MR8C1; PR8C2; FOR (inferredBy_MotIfSimilarity). HSF1; HSF2; HSF4 (inferredBy_MotIfSimilarityOrthology). MOTSC1; HR8C2 (inferredBy_MotIfSimilarity).	3.23 3.19 3.19 3.19 3.19 3.17
tapale_tr_pais_HOX82_SOX15_ACAAWKSNNNNMATA_CAP_repr fictorbook_HPS1 cibpM2351 hccomcetANDR_MOUSE.H11MC0.A tapale_AR_DBD_RBGWACANINHTGTWCY	HOXR2; SOX15 (directAnnotation). HSF1 (directAnnotation). AR (inferredBy_Orthology). AR (directAnnotation).	HOX82; H572; H574 (inferredby_MotifSimilarity); ME72A ME72C (inferredby_MotifSimilarity); COXA1; N83C1: N84C2; PGR (inferredby,MotifSimilarity); H571; H572; H574 (inferredby_MotifSimilarity); Orthology) N83C1; N83C2 (inferredby_MotifSimilarity); N83F1; CB8Pc; CE81; CC7; E276; SEAA, E214; HDAC2; MAX; MXI1; MYC; NELFE; N8F1; POLR2A;	3.23 3.19 3.19 3.19 3.19 3.17
tapale_tr_pais_HOX82_SOX15_ACAAWRSNNNNWATA_CAP_repr tectrobook_HPS1 citbp_M2351 hocomece_ANDR_MOUSEH11M0.0.A tapale_AR_DBD_RRGWACANNNTGTWCY dbcorrdb_HA-E2F1_ENCSR000EVM_1_m1	HOX82; SOX15 (directAnnotation). HSF1 (directAnnotation). AR (inferredBy_Orthology). AR (directAnnotation). E2F1 (directAnnotation).	HOX82; H572; H574 (inferredby, Motifsimilarity). MT97A, MH972 (inferredby, MotifSimilarity). FOXA1; NR3C1; NR3C2; GRG (inferredby, MotifSimilarity). H571; H572; H574 (inferredby, MotifSimilarity,Orthology). NR3C1; NR3C2 (inferredby, MotifSimilarity). BR51; CB8P5; CBR52; CBR52; SR2E4724; PUAC2; MAX; M011; MYC; NELFE; NR51; POLR2A; RAD21; NB8P5; SMARCA4; SR3E47; SR3E472; RM52; ZM274 (inferredby MotifSimilarity).	3.23 3.19 3.19 3.19 3.17 3.17
taplate_tr_paisHOX82_SOX15_ACAAWRSNNNNWATA_CAP_repr factorbook_HSF clubp_M2351 hocomoco_ANDR_MOUSE.H11M0.0.A taplate_AR_DBD_RRGWACANINITGTWCY dbcorrdb_HA-E2F1_ENCSR000EVM_1_m1 dbcorrdb_POLR2A_ENCSR000EVM_1_m12	HOX82, SOX15 (directAnnotation). HSF1 (directAnnotation). AR (inferredBy_Orthology). AR (directAnnotation). E2F1 (directAnnotation). POLR2A (directAnnotation).	HCX82; HS72; HS74 (inferredBy_MotifSimilarity). ME72A; ME72C (inferredBy_MotifSimilarity). TCXA1; NB3C1; NB3C2; PCR (inferredBy_MotifSimilarity). HS71; HS72; HS74 (inferredBy_MotifSimilarityOrtHolga). NB3C1; NB3C2 (inferredBy_MotifSimilarity). BB31; CB3P2; CB3C; CB3C; CF2; FS7; SB34; ZV32; CH3C2; MAX; MX01; MYC; NELFE; NB51; POLR2A; RAD21; RB3P5; SMACA4; S8EB51; SREB52; XRCC4; ZMI21; ZNF274 (inferredBy_MotifSimilarity).	3.23 3.19 3.19 3.19 3.17 3.17 3.17
tapiat_tpais_HOX82_S0X15_ACAAWRSNNNNMATTA_CAP_repr factbob_HS1 citbp_mX2511 hccomoc_ANDR_MOUSE H11M0.0.A tapale_AR_DB0_RRGWACANNNTGTWCY dbcordb_HA42F1_ENCSR000EVM_1_m1 dbcordb_U042A_ENCSR000A0Jm12 hdpi_PSMA6	HOXR2; SOX15 (directAnnotation). HSF1 (directAnnotation). AR (inferredBy_Orthology). AR (directAnnotation). E2F1 (directAnnotation). PSMA6 (directAnnotation). PSMA6 (directAnnotation).	HCX82; H572; H574 (inferredby_Motifsimilarity); ME72A, ME72C (inferredby_Motifsimilarity); COXA1; M83C1; M82C2 (inferredby_Motifsimilarity); H571; H572; H574 (inferredby_MotifSimilarity_Onthology); M871; CH882C; Inferredby_MotifSimilarity); B871; CH892; CH87; E576; SSRA; C272; HOAC2; MAY; MO11; MYC; NELFE; NBF1; POLR2A; R021; B887; CH89; C585; SSRA; C272; HOAC2; MAY; MO11; MYC; NELFE; NBF1; POLR2A; R021; B887; CM80; CAS; SSRB;	3.23 3.19 3.19 3.19 3.17 3.17 3.17 3.17 3.16
tapale_tr_joins_HOX82_SOX15_ACAAWRENNINYMATTA_CAP_repr factorbook_HPS1 cibp_M2351 hccomace_ANDR_MOUSE.H11MO.0.A tapale_AR_DBD_RRGWACANINYTGTWCY dbcorrdb_HA4271_ENCSR000RVM_1_m1 dbcorrdb_P0LR2A_ENCSR000A0J_1_m12 hdpi_pPSM6 japar_MA0591.1	HOX82, SOX15 (directAnnotation). HSF1 (directAnnotation). AR (inferredBy_Orthology). AR (directAnnotation). E2F1 (directAnnotation). POIRA2 (directAnnotation). POIRA2 (directAnnotation). MAFK (inferredBy_Orthology).	HOX82; H572; H574 (inferredby_MotifSimilarity); MR72A, MB72 (inferredby_MotifSimilarity); COXA1; NB321; H872; PGR (inferredby_MotifSimilarity); H571; H572; H574 (inferredby_MotifSimilarity_O-Orthology); NB3C1; NB3C2 (inferredby_MotifSimilarity); BB3C1; RBB3C; CGB4C; CB21; ESA2; H5A2; H5A2; H5A2; MAX1; MX11; MTC; NLFE; NBF1; POLR24; NA021; NBB45; SMACA4; SKB45; SKEB52; MCC4; ZM421; ZM274 (inferredby_MotifSimilarity); BBACH; BACH2; POS; FO38; FO31; FO32; JUN; JUNB; JUND; MAF; MAFB; MAFF; MAFG; MBF2A; NF22; NF221; NF221; SF231; SMARCC2 (inferredby_MotifSimilarity);	3.23 3.19 3.19 3.19 3.17 3.17 3.17 3.17 3.16 3.16
tapale_tpals_HOX82_SOX15_ACAAWRSNNNNMATTA_CAP_repr factorbook_HSS cibp_M2351 hocomoco_ANDR_MOUSE.H11M0 0.A tapale_AR_DB0_RRGWACANNNTGTWCY dbcorrdb_P0L82A_ENCSR000EVM_1_m1 dbcorrdb_P0L82A_ENCSR000EVM_1_m1 dbcorrdb_P0L82A_ENCSR000EVM_1_m1 dbcorrdb_P0L82A_ENCSR000EVM_1_m1 dbcorrdb_P0L82A_ENCSR00EVM_1_m1	HOX82, SOX15 (directAnnotation). HSF1 (directAnnotation). AR (inferredBy_Orthology). AR (directAnnotation). POLR2A (directAnnotation). POLR2A (directAnnotation). PSMA6 (inferredBy_Orthology).	HOX82; H572; H574 (inferredBy_MotifSimilarity). ME72A, ME72C (inferredBy_MotifSimilarity). FOXA1; MR31; H872; H574; CD PGR (inferredBy_MotifSimilarity). H571; H572; H574 (inferredBy_MotifSimilarityOPHology). NIR3C; H872C (inferredBy_MotifSimilarity). BB71; EDB76; CB87; CB72; ED73; ED87; ED82; JARC2; MAX1; MIC; NILF; NB71; POLR2A; MA22; HB97; SMACA4; SB871; SB8F2; XREC4; ZVM21; ZV#274 (inferredBy_MotifSimilarity). BACH1; BACH2; FOS; FOSB; FOS1; FOS1; JUN; JUNR; JUNR; MAF; MAF5; MAF6; ME72A; MF22; MF211; NF212; NF213; SMARCC2 (inferredBy_MotifSimilarity).	3.23 3.19 3.19 3.19 3.17 3.17 3.17 3.16 3.16 3.15
tapiate_tr_pairs_HOX82_SOX15_ACAAWRISNNNNMATTA_CAP_repr factorbook_HPS_ factorbook_HPS_ hecomococ_ANDR_MOUSE H11M0.0.A tapale_AR_DBO_RRSWACANNNTGTWCY decordb_PLAE2F1_ENCSR0000EVA_1_m1 decordb_PLAE2F1_ENCSR0000EVA_1_m1 decordb_PLAE2_ACSS000A00J_1_m12 hdpi_PSMA6 tapate_MX05511 perform_InVAUIT986 transfer_prc_M07100 decordb_PLAE2F1_ENCSR000EVB_1_m1	HOXR2; SOX15 (directAnnotation). HST2 (directAnnotation). AR (inferredBy_Orthology). AR (directAnnotation). PSMAG (directAnnotation). PSMAG (directAnnotation). MAFK (inferredBy_Orthology). HST2 (directAnnotation).	HCX82; H572; H574 (inferredby_MottSimilarity); ME72A, IME72 (inferredby_MottSimilarity); KOXAL, IM821; H812; CPR (inferredby_MottSimilarity); H571; H572; H574 (inferredby_MottSimilarity_Onthology); MB71; CB82; CB82; CB72; CF87; ES8A; CF72; CF74; MB71; CB82; CB82; CF75; CF75; ES8A; CF74; CF74; MottSimilarity); B84; LCB82; CF75; CF75; ES8A; CF74; CF74; CF74; Inferredby_MottSimilarity); B84; LCB82; KF74; CF74; SF84; CF74; CF74; CF74; CF74; CF74; MottSimilarity); B84; LCF74; F62; CF75; F058; F051; F052; JUN; IUNB; IUND; M4F; MAFB; MAFF; MAFG; MEF24; NF22; NF21; JF721; JF7213; SMARCC1 (inferredby_MottSimilarity); HCX82; VF72; IF54; (inferredby_MottSimilarity); HCX82; VF73; IF54; (inferredby_MottSimilarity); HCX82; VF74; (inferredby_MottSimilarity); HCX82; VF74; (inferredby_MottSimilarity); HCX82; VF74; (inferredby_MottSimilarity); HCX82; VF74;	3.23 3.19 3.19 3.19 3.17 3.17 3.17 3.16 3.16 3.15 3.15 3.15
tapiate_tr_pairs_HOX82_SOX15_ACAAWRISNNNNMATTA_CAP_repr factorbook_HPS1 citbp_M2251 hccomoco_ANDR_MOUSE H11M0.0.A tapale_AR_DB0_RRGWACANNNTGTVCY dbcordb_HAC2F1_ENCS8000A01_1_m1 dbcordb_UR32Q_ENCS8000A01_1_m12 hdpi_PS3M6 japar_MA0591.1 preferm_mrMotf1986 tranfat_pr=_0M20000BHE_1_m1 homer_AGAACARCTGTTCT_ARE	HOX82, SOX15 (directAnnotation). HSF1 (directAnnotation). AR (inferredBy_Orthology). AR (directAnnotation). POB2A2 (directAnnotation). POB2A2 (directAnnotation). PSM46 (directAnnotation). HSF1 (directAnnotation). NA3C1 (directAnnotation). NA3C1 (directAnnotation).	HCX82; H572; H574 (inferredBy_MotifSimilarity); MR72A, MB72 (inferredBy_MotifSimilarity); COXA1; MB21; HB72 (inferredBy_MotifSimilarity); H571; H572; H574 (inferredBy_MotifSimilarity_, Orthology); MB71; CB89; CB89; CG75; F256; SS8A; E374; HCA2; MAX; MXI1; MYC; NGFE, NRF1; POLR2A; RD21; RB82B; MS45; SMACA4; SRE8F1; SRE8F2; MCC4; ZM21; ZW274 (inferredBy_MotifSimilarity); BACH1; BACH2; FOS; FOS8; FOS1; FOS12; JUN; JUNB; JUND; MAF; MAFB; MAFF; MAFG; MEF2A; NF2; NF221; HF221; NF221; SMACC2 (inferredBy_MotifSimilarity); HCX82; H572; H574 (inferredBy_MOtifSimilarity);	3.23 3.19 3.19 3.19 3.17 3.17 3.17 3.16 3.16 3.15 3.15 3.15 3.15 3.14
tapale_tpains_HOX02_SDIS_ACAAWRENNINYMATTA_CAP_repr factorbook_HPS_ citbp_M2351 hccomocc_ANDR_MOUSE H11MO.0.A tapale_AR_DBD_RRGWACANINYTGTWCY dbcorrdb_NA4251_ENCSR000RVM_1_m1 dbcorrdb_P0LR2A_ENCSR000RVM_1_m1 dbcorrdb_P0LR2A_ENCSR000RVM_1_m1 dbcorrdb_P0LR2A_ENCSR000RVM_1_m1 dbcorrdb_UR361_ENCSR000RVM_1_m1 dbcorrdb_UR361_ENCSR000RVM_1_m1 dbcorrdb_UR361_ENCSR000RVM_1_m1 dbcorrdb_UR361_ENCSR000RVM_1_m1 dbcorrdb_UR361_ENCSR000RVM_1_m1	HOX82, SOX15 (directAnnotation). HSF1 (directAnnotation). AR (inferredBy_Orthology). AR (directAnnotation). POLR2A (directAnnotation). POLR2A (directAnnotation). MAFK (inferredBy_Orthology). HSF1 (directAnnotation). NR3C1 (directAnnotation). AR (directAnnotation). AR (directAnnotation).	HOX82; H572; H574 (inferredby_Motifismilarity); M072A, MB72 (inferredby_Motifismilarity), COXA1; NB32: H582; Clofkerredby_Motifismilarity), H571; H572; H574 (inferredby_Motifismilarity_O-Orthology), NB3C1; NB3C2 (inferredby_Motifismilarity), BB71; CB89; CCB7; CE76; E576; SB8A; CE72; HDAC2; MAX; MX11; MTC; NLF; NB71; POLR2A; MO21; MB89; SMACA4; SB81; STCF1; E276; SB8A; CE72; HDAC2; MAX; MX11; MTC; NLF; NB71; POLR2A; MO21; MB89; SMACA4; SB81; STCF1; E276; SB8A; CE72; HDAC2; MAX; MX11; MTC; NLF; NB71; POLR2A; MO21; MB89; SMACA4; SB81; STCF1; SB81; STCF2; MAX; HDAC2; MAX; MX11; MTC; NLF; NB71; POLR2A; MO21; MB89; SMACA4; SB81; STCF1; SB81; STCF2; MAX; HDAC2; MAX; MX11; MTC; NLF; NB71; POLR2A; MO22; H572; J1; FE72; J1; FE72; SMACC2 (inferredby_Motifismilarity). HCX82; H572; H574; Inferredby_Motifismilarity). FXX41; NB3C1; PG8 (inferredby_Motifismilarity).	3.23 3.19 3.19 3.17 3.17 3.17 3.17 3.16 3.16 3.15 3.15 3.15 3.15 3.14 3.14
tapide_tr_pais_HOX2_SOUIS_ACAAWKISNNNNMATTA_CAP_repr factorbook_HIPS factorbook_HIPS factorbook_HIPS tapide_nR_DBO_RRAUSE HI1MO.0.A tapide_nR_DBO_RRAWKANNNTGTWCY decordb_PLAE2F1_ENCSR0000EVM_1_m1 decordb_PLAE2F1_ENCSR0000EVM_1_m1 decordb_PLAE2F1_ENCSR0000EVM_1_m1 decordb_PLAE2F1_ENCSR000EVM_1_m1 decordb_RAE2F1_ENCSR000EVM_1_m1 http://www.secordbattable.com/seco	HOXR2;250(15) (directAnnotation). HST2 (directAnnotation). AR (inferredBy_Orthology). AR (directAnnotation). PSMA6 (directAnnotation). PSMA6 (directAnnotation). MAFK (inferredBy_Orthology). HST2 (directAnnotation). NR3C1 (directAnnotation). PSXF2 (directAnnotation). PSXF2 (directAnnotation). PSXF2 (directAnnotation). PSXF2 (directAnnotation). PSXF2 (directAnnotation).	HOK82; H572; H574 (inferredby_MotifSimilarity). ME72A, ME72C (inferredby_MotifSimilarity). FOXA1; NBC1: NBC2; PGR (inferredby_MotifSimilarity). HS72; NBS2; Informedby_MotifSimilarity). BS7; HS82C (inferredby_MotifSimilarity). BS7; HS82C (inferredby_MotifSimilarity). BS7; HS82C (inferredby_MotifSimilarity). BS7; HS82C (inferredby_MotifSimilarity). HS72; NF22; H574 (inferredby_MotifSimilarity). HS72; NF22; H574 (inferredby_MotifSimilarity). HS72; NF22; H574 (inferredby_MotifSimilarity). HS72; H574; Inferredby_MotifSimilarity). FOXA2; H574 (inferredby_MotifSimilarity). FOXA2; H574 (inferredby_MotifSimilarity). FOXA2; H574 (inferredby_MotifSimilarity). FOXA2; H574 (inferredby_MotifSimilarity). FOXA1; NB3C; PGR (inferredby_MotifSimilarity). FOXA1; PSR2; PAS9 (inferredby_MotifSimilarity). FOXA1; FSR2; PAS9 (inferredby_MotifSimilarity).	3.23 3.19 3.19 3.17 3.17 3.17 3.16 3.16 3.15 3.15 3.15 3.15 3.14 3.14 3.14 3.13
tapiate_trains_t	HOX82, SOX15 (directAnnotation). HST1 (directAnnotation). AR (inferredBy_Orthology). AR (directAnnotation). PSMA6 (directAnnotation). PSMA6 (directAnnotation). MAFK (inferredBy_Orthology). HST1 (directAnnotation). FOX71 (directAnnotation). FOX71 (directAnnotation). PXX6 (directAnnotation). PXX6 (directAnnotation). FOX71 (directAnnotation).	HCX82; H572; H574 (inferredby_MottSimilarity). ME72A, ME72 (inferredby_MottSimilarity). FCXA1, M832; H822; R6167redby_MottSimilarity). M8475; M842; M842; M842; M843; M844;	3.23 3.19 3.19 3.17 3.17 3.17 3.17 3.16 3.16 3.16 3.15 3.15 3.15 3.15 3.14 3.14 3.14 3.13 3.13 3.12
tapiate_trains_t	HOX82; SOX15 (directAnnotation). HST2 (directAnnotation). AR (inferredBy_Orthology). AR (directAnnotation). POLR2A (directAnnotation). POLR2A (directAnnotation). MAFK (inferredBy_Orthology). HST2 (directAnnotation). N33C1 (directAnnotation). POXP2 (directAnnotation). POXP2 (directAnnotation). POXP2 (directAnnotation). POXP2 (directAnnotation). POXP2 (directAnnotation). POXP2 (directAnnotation). POXP2 (directAnnotation). POXP2 (directAnnotation). POXP2 (directAnnotation).	HOX82; H572; H574 (InferredBy_MottISimilarity). ME72A, ME72 (InferredBy_MottISimilarity). COXA1; M821; H822 (InferredBy_MottISimilarity), M951; H572; H574 (InferredBy_MottISimilarity_O-Orthology). M873(; H832) (InferredBy_MottISimilarity). B871; CEBPB; CREB1; CTCF; E2F6; ESRA, E2H2; HDAC2; MAX; MXI1; MTC; NG.FE; NRF1; POLR2A, M021; M895; ISMACH; SRB47; JSREP2; MCC4; ZMC1; ZW274 (InferredBy_MottISimilarity). BACH1; EACH2; FCS; FCSB; FOSB; FOS1; FCS1; FCSB; ZMC2; ZMC2; MAX; MXI1; MTC; NG.FE; NRF1; POLR2A, M22; NF221; H574; InferredBy_MottISimilarity). BACH1; EACH2; FCS; FCSB; FOSB; FOS1; FCSC2; JUN; JUNB; JUND; MAF; MAFB; MAFF; MAFG; MEF2A, NF22; NF221; H574 (InferredBy_MottISimilarity). HCX82; HS72; H574 (InferredBy_MottISimilarity). FCX41; FRA31; FCB (InferredBy_MottISimilarity). FCX41; FAX2; FCFC1; InferredBy_MottISimilarity). EF21; EAX4; FGC; InferredBy_MottISimilarity). EF11; EAX4; FGC; InferredBy_MottISimilarity). EF12; EAX4; FGC; InferredBy_MottISimilarity).	3.23 3.19 3.19 3.17 3.17 3.17 3.17 3.16 3.16 3.15 3.15 3.15 3.15 3.15 3.14 3.13 3.13 3.12 3.12
tapide_tr_pais_HOX2_SOI3_ACAAWESNNNNMATA_CAP_repr factorbook_HP31 citbg_LAP_20151 hccomoco_ANDR_MOUSE.H11MO.0.A tapide_AR_DB0_RROWSKANNNTKOTWCYY dbcordb_P0182A_ENCSR000EVM_1_m1 dbcordb_P0182A_ENCSR000EVM_1_m12 hdpl_PSMA6 lipapur_MAXD511.1 prefermnrMwEt1986 transfar_prM07100 dbcordb_B02166 transfar_prM03573 hccomoco_EX3_HUMAN.H11MO.0.C hccomoco_EX3_HUMAN.H11MO.0.C	HOXR2;250(15) (directAnnotation), HST2 (directAnnotation), AR (inferredBy_Orthology), AR (directAnnotation), PSMA6 (directAnnotation), PSMA6 (directAnnotation), MAFK (inferredBy_Orthology). HST2 (directAnnotation), NASC1 (directAnnotation), PXM21 (directAnnotation), PXM24 (directAnnotation), PXM26 (dire	HOX82; H572; H574 (inferredby_MottSimilarity); MT2A, ME32; M574 (inferredby_MottSimilarity), GYGAII, NB32; H584; CPGR, Defredby, MottSimilarity), H572; H574; M572; H574 (inferredby_MottSimilarity, Orthology), NB32; H587; GSBP; GSBB; CFG; F276; GSBA; CA2; H542; M574; M571; M572; H574 (inferredby_MottSimilarity), BB7; GSBP; GSBB; CFG; F276; GSBA; CA2; H542; M542; M547; M517; POLR24; M022; M587; M587; M547; M547	3.23 3.19 3.19 3.17 3.17 3.17 3.16 3.16 3.16 3.15 3.15 3.15 3.15 3.14 3.14 3.13 3.13 3.12 3.12
tapiate_trains_HOX82_S013_ACAAWRISNNNNATTA_CAP_repr factorbook_HP31 citbg_m24251 hocomoco_ANDR_MOUSE H11M0.0.A tapiate_AR_DB0_RRSWACANNNTGTVCYY decordb_HA-E2F1_ENCSR000EVM_1_m1 decordb_P0142_ACSF1_ENCSR000EVM_1_m12 hdpi_P5MA6 ispar_MW05511 performnNAU11986 trainfac_pro_M05106 fbcordb_B012_ENCSR000AH_1_m1 home_AGAAARCCGTCTCT_ARE trainfac_pro_M05166	HOXR2; SOX15 (directAnnotation). HST2 (directAnnotation). AR (inferredBy_Orthology). AR (directAnnotation). PSMAG (directAnnotation). PSMAG (directAnnotation). MAFK (inferredBy_Orthology). HST1 (directAnnotation). MAFK (inferredBy_Orthology). HST2 (directAnnotation). PSMS1 (directAnnotation). PSMS1 (directAnnotation). PSM5 (directAnnotation). PDM51 (directAnnotation). PDM51 (directAnnotation). PDM51 (directAnnotation). PDM51 (directAnnotation). PDM51 (directAnnotation). PDM51 (directAnnotation). PDM51 (directAnnotation). PDM51 (directAnnotation). PDM52 (directAnnotation).	HCX82; H572; H574 (inferredby, MottiSimilarity), ME72A, ME72 (inferredby, MottiSimilarity), FCXA1, M832; H452; Related State, 2008; MottiSimilarity), ME72A, M832; Interedby, MottiSimilarity), M847; CH882; CH82; CH72; F254; CH88A; CH72; HCA2; MA3; M011; MM2; M817; M878; M847; CH882; CH82; CH72; F254; CH88A; CH72; HCA2; MA3; M011; MM2; M114; M617; M124; M618; CH147; SH847; SH847; CH24; CH421; 2N274 (inferredby, MottiSimilarity), BACH1; BACH2; F055; F058; F051; F051; F052; JUN; JUNB; JUND; M4F; MAFB; MAFF; MAFG; MEF2A; MF22; NF221; MF212; NF221; SM48CC1 (inferredby, MottiSimilarity), BACH1; BACH2; F05; F058; F051; F051; F051; JUN; JUNB; JUND; M4F; MAFB; MAFF; MAFG; MEF2A; MF22; NF221; NF212; NF221; SM48CC1 (inferredby, MottiSimilarity), BACH1; BACH2; F06; (inferredby, MottiSimilarity), BACH1; BACH2; F06; (inferredby, MottiSimilarity), E171; ELA1; E06; (inferredby, MottiSimilarity), E172; ELA1; F06; (inferredby, MottiSimilarity), E172; ELA1; F06; (inferredby, MottiSimilarity), E172; ELA1; F074; F0704; F0704; F074;	3.23 3.19 3.19 3.17 3.17 3.17 3.17 3.16 3.15 3.15 3.15 3.15 3.14 3.14 3.13 3.13 3.12 3.12
tapale_tpains_HOX2_SOI3_ACAAWRISNNNNMATTA_CAP_repr factorbook_HP31 citbpN2251 hccomoco_ANDR_MOUSE H11M0.0.A tapale_AR_DB0_RRGWACANNNTGTVCY dbcordbHAC2F1_ENCSR0000EVM1_m1 dbcordb_UA22F1_ENCSR000A0J3_m12 hdpi_P5M46 lapar_MA0591.1 prefer_m_mMotf1386 transfs.prM03216 transfs.prM03216 transfs.prM03216 transfs.prM03213	HOX82, SOX15 (directAnnotation). HSF1 (directAnnotation). AR (inferredBy_Orthology). AR (directAnnotation). POID2A (directAnnotation). PSMA6 (directAnnotation). MAFK (inferredBy_Orthology). HSF1 (directAnnotation). N33C1 (directAnnotation). PAX6 (directAnnotation). PAX6 (directAnnotation). POXF1 (directAnnotation). POXF1 (directAnnotation). POXF1 (directAnnotation). POXF1 (directAnnotation). POXF1 (directAnnotation). POXF2 (direct	HCX82; H52; H54 (InferredBy_MotifSimilarity); MIE2A, ME22 (InferredBy_MotifSimilarity), COXA1, H821; H822 (RiferredBy_MotifSimilarity), MIE3A, ME22 (RiferredBy_MotifSimilarity), MIE3A, ME32 (RiferredBy_MotifSimilarity), ME42, ME32 (RiferredBy_MotifSimilarity), ME41; MACH2; F05; F058; F051; F051; SIRA, EX2; H0A2; MAX, MU1; MC; NE4E; NRF1; P04R2A, M22; NRE21; NRF21; RF51; SIRBF2; NRC47; ZXR21; ZVR274 (MirredBy_MotifSimilarity), ME41; MACH2; F05; F058; F051; F051; SIRA, EX2; H0A2; MAX, MU1; MC; NE4E; NRF1; P04R2A, M22; NRF21; NFE21; NFE21; SIRBF2; MICC4; ZMI2; ZVR274 (MirredBy_MotifSimilarity), MACH2; NRF21; HF21; NFE21; SIRBF2; MotifSimilarity), MAX; TAX1; F63 (InferredBy_MotifSimilarity), F0X4; F13; F03; F04FredBy_MotifSimilarity), F0X4; F14; F14; F16; InferredBy_MotifSimilarity), F1726; F125; T474; T98 (InferredBy_MotifSimilarity), F1726; F125; T474; T98; InferredBy_MotifSimilarity), F0X4; F0X4; F0X1; F0X1; F0X1; F0X2; F0X2; F0X2; F0X2; F0X1; F0X1; F0X1; F0X4; F0X3; F0X3; F0X3; F0X3; F0X4; F0X4; F0X4; F0X4; F0X1; F0X2; F0X1; F0X2; F0X	3.23 3.19 3.19 3.17 3.17 3.17 3.17 3.16 3.15 3.15 3.15 3.14 3.14 3.14 3.13 3.12 3.12 3.12 3.12
tapale_tpains_HOX2_SOI3_ACAAWRISNNNNMATTA_CAP_repr factorbook_HP31 cibpM2351 hecomocoANDR_MOUSE H11M0.0.A tapale_AR_DBD_RRGWACANNNTGTWCY dbcordbHAC271_ENCSR000A0J_1_m12 dbcordb_POIR2A_ENCSR000A0J_1_m12 heptM2591.1 prefermMMOUF1986 transfs_pro_M00591.1 prefermMMOUF1986 transfs_pro_M00526 transfs_pro_M00526 transfs_pro_M00573 hecomocoPXKS_HUMAN H11M0.0.C hecomocoPXKS_HUMAN H11M0.0.D dcordb_POIR2A_ENCSR000AH_1_m1	HOX82, SOX15 (directAnnotation). HSF1 (directAnnotation). AR (inferredBy_Orthology). AR (directAnnotation). POLR2A (directAnnotation). POLR2A (directAnnotation). MAFK (inferredBy_Orthology). HSF1 (directAnnotation). NR3C1 (directAnnotation). FOXF1 (directAnnotation). FOXF1 (directAnnotation). POXE1 (directAnnotation).	HOX82; H572; H574 (InferredBy_MotifSimilarity). ME72A, ME72 (InferredBy_MotifSimilarity). COXA1, M821; H872 (InferredBy_MotifSimilarity), H571; H572; H574 (InferredBy_MotifSimilarity_O-Orthology). M832; H872 (InferredBy_MotifSimilarity). B871; CB8P6; CR685; CTCF; E2F6; ESRA, C2H2; HDAC2; MAX; MXI1; MTC; NLFE; NRF1; POLR2A; M021; M882; GM875; SMACA4; SAB471; SK8B72; MCCG; ZM62; MAX; MXI1; MTC; NLFE; NRF1; POLR2A; M021; M882; GM875; SMACA4; SAB471; SK8B72; MCCG; ZM62; MAX; MXI1; MTC; NLFE; NRF1; POLR2A; M021; M897; SMACA4; SAB471; SK8B72; MCCG; ZM62; ZM87; M021; M697; SMACA4; SAB47; SK8B72; MCCG; ZM62; ZM87; MCK2; NF521; H574 (InferredBy_MotifSimilarity). HOX82; H552; H574 (InferredBy_MotifSimilarity). FOXA1; R06; CI1 (InferredBy_MotifSimilarity). FOXA1; R06; CI1 (InferredBy_MotifSimilarity). FOXA1; R06; FOXB; FOXE; FOXA; FOXA2; FOX3; FOX1;	3.23 3.19 3.19 3.17 3.17 3.17 3.16 3.15 3.15 3.15 3.14 3.14 3.14 3.13 3.12 3.12 3.12 3.12
tapidie_tpains_HOX2_SOI3_ACAAWRENNINYMATTA_CAP_repr factorbook_HP31 citubg_MC2511 hocomoco_ANDR_MOUSE H11M0.0 A tapide_AR_DB0_RROWGENINTGTWCYY dbcordb_PLAE2F1_ENCSR000EVM_1_m1 dbcordb_PLAE2F2_ENCSR000EVM_1_m12 hdpl_PSMA6 lipapr_MM0591.1 prefermnrMw101896 transfs_pro_M07100 dbcordb_PC2166 transfs_pro_M07206 transfs_pro_M07373 honew_L6AACASHCTGTCTT_ABE transfs_pro_M059216 transfs_pro_M059216 transfs_pro_M059216 transfs_pro_M059216 transfs_pro_M059216 transfs_pro_M059216 transfs_pro_M059216 transfs_pro_M059216 transfs_pro_M059216 transfs_pro_M059216 transfs_pro_M059216 transfs_pro_M05931	HOXR2; 25043 (directAnnotation). HST2 (directAnnotation). AR (inferredBy_Orthology). AR (directAnnotation). PSMAG (directAnnotation). PSMAG (directAnnotation). MAFK (inferredBy_Orthology). HST2 (directAnnotation). NASC1 (directAnnotation). PSMAG (directAnnotation). PSMAG (directAnnotation). POR24 (directAnnotation). POR24 (directAnnotation). POR24 (directAnnotation). POR24 (directAnnotation). POR24 (directAnnotation).	HCK82; H572; H574 (inferredby, MotifSimilarity), ME72A, ME72 (inferredby, MotifSimilarity), ME72A, M572; M574; CPG (inferredby, MotifSimilarity), M574; M572; M574; M574; M574; M574; M574; M572; M574 (inferredby, MotifSimilarity), B671; B620; M572; M574; M574; S58A; Z274; M574; M571; M572; M574 (inferredby, MotifSimilarity), B671; B620; M572; M574; M574; S58A; Z274; M572; M574;	3.23 3.19 3.19 3.17 3.17 3.17 3.17 3.17 3.17 3.16 3.16 3.15 3.15 3.15 3.15 3.14 3.14 3.13 3.12 3.12 3.10 9 3.09
tapiat_plais_HOX2_SOI3_ACAAWSISNINIMATIA_CAP_repr factorbook_HP31 cisbp_LA2251 hecomoco_ANDR_MOUSE H11M0.0.A tapale_AR_DB0_RRSWACANINITGTVCYY decordb_HA-C2F1_ENCSR000EVM_1_m1 decordb_P0182A_ENCSR000EVM_1_m1 hdpi_PSMA6 lapar_MA05511 begin_M05510 tranite_pro_M05216 tranite_pro_M05216 tranite_pro_M05216 tranite_pro_M05216 tranite_pro_M05216 tranite_pro_M05217 hecomoco_FX6_HUMAN_H11M0.0.C hecomoco_FX6_HUMAN_H11M0.0.D decordb_P0182A_ENCSR000ALH_1_m1 cibp_M0747 tranite_pro_M06871	HOX82, SOX15 (directAnnotation). HST2 (directAnnotation). AR (inferredBy_Orthology). AR (directAnnotation). PSMA6 (directAnnotation). PSMA6 (directAnnotation). MAFK (inferredBy_Orthology). HST1 (directAnnotation). MARK (inferredBy_Orthology). HST1 (directAnnotation). PAX6 (directAnnotation). PAX6 (directAnnotation). PAX6 (directAnnotation). POXT1 (directAnnotation). POXT1 (directAnnotation). POXT1 (directAnnotation). POXT2 (directAnnotation). POXR1 (directAnnotation). POLR2A (directAnnotation). POLR2A (directAnnotation). POLR2A (directAnnotation).	HCX82; H52; H54 (InferredBy_MottSimilarity). ME22, ME22 (InferredBy_MottSimilarity). ME23, ME22 (InferredBy_MottSimilarity). ME23, ME22 (InferredBy_MottSimilarity). ME21, ME22 (InferredBy_MottSimilarity). ME21, ME22 (InferredBy_MottSimilarity). ME21, ME22 (InferredBy_MottSimilarity). ME21; ME23, CH22, L55; FOSB, FOS1; FOS2; UN; UNB; UND; MAF; MAF5; MAF5; ME72, ME22, ME22, ME21; InferredBy_MottSimilarity). ME21; ME21; ME21; ME21; ME21; SteBr2; MICC4; ZMI2; ZME274 (InferredBy_MottSimilarity). ME21; InferredBy_MottSimilarity). ME21; ME21; ME21; ME21; MME21; MME2(InferredBy_MottSimilarity). HCX82; H52; H544 (InferredBy_MottSimilarity). FCX4; FMS2; FOSF (InferredBy_MottSimilarity). FCX4; FMS2; FASF (InferredBy_MottSimilarity). FCX4; FMS2; FASF (InferredBy_MottSimilarity). FCX4; FMS2; FOS1; FOS1; FCM3; FCM3	3.23 3.19 3.19 3.17 3.17 3.17 3.17 3.17 3.17 3.16 3.16 3.15 3.15 3.15 3.15 3.15 3.12 3.12 3.12 3.12 3.12
tapale_tpains_HOX2_SOI3_ACAAWRISNNNNMATTA_CAP_repr factorbook_HP31 citbpM2251 hccomocoANDR_MOUSE.H11MO.0.A tapale_AR_DB0_RRGWACANNNTGTWCY dbcordbHAC271_ENCS80000EVM_1_m1 dbcordb_UA0274_ENCS8000A01_1_m12 hdpi_pP3M6 dbcordb_P0LR2A_ENCS8000A01_1_m12 hdpi_pP3M6 famer_AGAACARGENTCTTARE transfs_pro_M0216 transfs_pro_M0373 hccomocoFAX6_HUMAW.H11MO.0.C hccomotoFAX6_HUMAW.H11MO.0.D dbcordb_P0LR2A_ENCS8000AU.1_m1 citbp_M07747 transfs_pro_M06871 transfs_pro_M0398	HOX82, SOX15 (directAnnotation). HST2 (directAnnotation). AR (inferredBy_Orthology). AR (directAnnotation). POLR2A (directAnnotation). POLR2A (directAnnotation). MAFK (inferredBy_Orthology). HST2 (directAnnotation). NR3C1 (directAnnotation). POXF2 (directAnnotation). NR3C1 (inferredBy_Orthology).	HCX82; H52; H54 (InferredBy_MottSimilarity). ME72A, ME72 (InferredBy_MottSimilarity). ME72A, ME72 (InferredBy_MottSimilarity). ME73A, ME72 (InferredBy_MottSimilarity). B871; CEBPB; CREB1; CTCF; E2F6; ESRA, E2H2; HDAC2; MAX; MKI1; MTC, NLFE; NRF1; POLR2A, M021; M822 (InferredBy_MottSimilarity). B871; CEBPB; CREB1; CTCF; E2F6; ESRA, E2H2; HDAC2; MAX; MKI1; MTC, NLFE; NRF1; POLR2A, M021; M822; M521; MAXCM; SREB1; SKEB2; XRCC4; ZML2; ZW274 (InferredBy_MottSimilarity). BACH1; EAACH2; FCS; FCSB; FOSB, FOS1; FOS2; JUN; JUNB; JUND; MAF; MAFB; MAFF; MAFG; MEF2A, MF2; NFE21; MF24; InferredBy_MottSimilarity). HCX82; HF521; M54 (InferredBy_MottSimilarity). HCX82; HS72; HF54 (InferredBy_MottSimilarity). FCX41; FAX2; FCB1; ME74; MCS1; FOX1; FCX2; FCX03; FCX4; FCX1; FCX2; FCXX;	3.23 3.19 3.19 3.17 3.17 3.17 3.16 3.16 3.15 3.15 3.15 3.15 3.14 3.14 3.14 3.13 3.12 3.09 3.09 3.09 3.09
tapide_tpids_HOX2_SOI3_ACAAVKSNNNNNNTACTA_CAP_repr factorbook_HP31 citbg_mC2511 hocomocg_ANDR_MOUSE.H11M0.0.A tapide_AR_DB0_RRKWLSNNTGTWCYY dbcordb_POL82_ENCSR0000EVM_1_m1 dbcordb_POL82_ENCSR0000EVM_1_m1 hdpi_PSMA6 lipapr_MMOS91.1 preferm_mrKwL19866 transfs_rpc_MO7100 dbcordb_POL82_ENCSR000BHE_1_m1 home_ACAACASYCTGTCTT_ARE transfs_rpc_MO82166 transfs_rpc_MO82166 transfs_rpc_MO82166 transfs_rpc_MO82166 transfs_rpc_MO82167 transfs_rpc_MO8871 transfs_rpc_MO8871	HOXR2; SOX15 (directAnnotation). HST2 (directAnnotation). AR (inferredBy_Orthology). AR (directAnnotation). PSMA6 (directAnnotation). PSMA6 (directAnnotation). MAFK (inferredBy_Orthology). HST2 (directAnnotation). RS21 (directAnnotation). PSX46 (directAnnotation). PSX46 (directAnnotation). POR24 (directAnnotation).	HCK82; H572; H574 (inferredBy_MottSimilarity). ME72A, IME27C (inferredBy_MottSimilarity). ME72A, IME27C (inferredBy_MottSimilarity). ME72A, IME27C (inferredBy_MottSimilarity). BR51; IME27; IM52 (inferredBy_MottSimilarity). BR51; IME27; IM52 (inferredBy_MottSimilarity). EXX1; IME21; IME21; IME213; IME21; IME17C (inferredBy_MottSimilarity). EXX1; IME21; IME21; IME213; IME213; IME15imilarity). EXX1; IME21; IME21; IME214; IME15imilarity). EXX1; IME21; IME1 (inferredBy_MottSimilarity). EXX1; IME21; IME1 (inferredBy_MottSimilarity). EXX1; IME21; IME1 (inferredBy_MottSimilarity). EXX1; IME21; IME21; IME216; IME216; IME15imilarity). EXX1; IME21; IME1 (inferredBy_MottSimilarity). EXX1; IME21; IME31; IME1 (inferredBy_MottSimilarity). EXX1; IME21; IME1 (inferredBy_MottSimilarity). EXX1; IME21; IME1 (inferredBy_MottSimilarity). EXX1; IME21; IME1 (inferredBy_MottSimilarity). EXX1; IME22; IME22; IME22; IME21; IME1] EXX1; IME22; IME22; IME21; IME1] EXX1; IME22; IME22; IME21; IME1] EXX1; IME22; IME22; IME22; IME1] EXX1; IME22; IME22; IME21; IME1] EXX1; IME22; IME22; IME22; IME22; IME22; IME22; IME2]; IME1] EXX1; IME22; IME22; IME22; IME22; IME2]; IME2]; IME2] EXX1; IME22; IME22; IME22; IME2];	3.23 3.19 3.19 3.17 3.17 3.17 3.16 3.15 3.15 3.15 3.15 3.15 3.14 3.14 3.14 3.13 3.12 3.09 3.09 3.09
tapiate_tpains_HOX2_SOI3_ACAAWRISINNINMATIA_CAP_repr factorbook_HP31 cistop_D_M2251 hccomocc_ANDR_MOUSE H11M0.0.A tapale_AR_DBD_RRSWACANINITGTVCYY decordb_HA-E2F1_ENCSR000EVM_1_m1 decordb_P014A_E2F1_ENCSR000EVM_1_m1 hdpi_PSMA6 HapsF_MA0551.1 prefermnfwA0F1586 transfs_pro_M0216 transfs_pro_M0216 transfs_pro_M0216 transfs_pro_M0216 transfs_pro_M0216 transfs_pro_M0216 transfs_pro_M0215 transfs_pro_M06871 Lansfs_pro_M068918 cisbp_M0747 transfs_pro_M068918 cisbp_M0715 transfs_pro_M089988 cisbp_M07165	HOX82; SOX15 (directAnnotation). HST2 (directAnnotation). AR (inferredBy_Orthology). AR (directAnnotation). PSMA6 (directAnnotation). PSMA6 (directAnnotation). MAFK (inferredBy_Orthology). HST2 (directAnnotation). AR3C1 (directAnnotation). PAX8 (directAnnotation). PAX8 (directAnnotation). POX71 (directAnnotation). NR3C1 (inferredBy_Orthology). NR3C1 (inferredBy_Orthology).	HCX82; H572; H574 (InferredBy_MotISImiliarity), ME72A, ME72 (InferredBy_MotISImiliarity), CXX1, H832; H574 (InferredBy_MotISImiliarity), ME72A, H572; H574 (InferredBy_MotISImiliarity), MB71; CH82; H572; H574 (InferredBy_MotISImiliarity), MB71; CH82; H572; H574 (InferredBy_MotISImiliarity), MCX1; B82; H572; H574 (InferredBy_MotISImiliarity), MCX1; PA3; FA3 (InferredBy_MotISImiliarity), MCX1; FA3; FA3 (InferredBy_MotISImiliarity), MCX1; FA3; H574;	3.23 3.19 3.19 3.17 3.17 3.17 3.17 3.17 3.17 3.17 3.17
tapiate_tpains_HOX2_SOI3_ACAAWRISNNNNMATTA_CAP_repr factorbook_HP31 citbpM2251 hccomoco_ANDR_MOUSE H11M0.0.A tapale_AR_DB0_RRGWACANNNTGTVCY dbcordb_HA22F1_ENCSR0000EVM_1_m1 dbcordb_DUR32_ENCSR000A0J3_m12 hdpi_P5M46 lapar_M40591.1 preferm_mMotf1386 transfr.prM07100 dbcordb_DUR32_ENCSR000A0HE1_m1 hmemAGACAGKTGTTCT_ARE transfr.prM0373 hccomoco_FX45_HUMAH111M0.0.D dbcordb_P0LR2A_ENCSR000ALH_3_m1 citbp_M0715 transfr.prM08998 citbp_M0716	HOX82, SOX15 (directAnnotation), HSF1 (directAnnotation), AR (inferredBy_Orthology), AR (directAnnotation), POID2A (directAnnotation), PSMA6 (directAnnotation), MAFK (inferredBy_Orthology), HSF1 (directAnnotation), RAGT1 (directAnnotation), PAX6 (directAnnotation), POX71 (directAnnotation), POX71 (directAnnotation), POX71 (directAnnotation), POX71 (directAnnotation), POX24 (directAnnotation), POX24 (directAnnotation), POX24 (directAnnotation), POX24 (directAnnotation), POX24 (directAnnotation), POX24 (directAnnotation), NR3C1 (inferredBy_Orthology), NF2L2 (directAnnotation), NATC3; SP11 (directAnnotation), NATC3; SP11 (directAnnotation),	HCX82; H52; H54 (inferredBy_MotifSimilarity), MIE2A, ME22 (inferredBy_MotifSimilarity), MIE2A, ME22 (inferredBy_MotifSimilarity), ME32, ME32 (inferredBy_MotifSimilarity), ME32, ME32 (inferredBy_MotifSimilarity), ME42, ME32 (inferredBy_MotifSimilarity), ME41; BACH2; FOS; FOSB; FOS1; FOS1; SERA, EX2; HOA2; MAX, MOI; MC; ME4E; NRF1; POLR2A, MA21; NB22; ME32; ME32; ME31; SEBF2; XRCC4; ZM21; ZW274 (inferredBy_MotifSimilarity), BACH1; BACH2; FOS; FOSB; FOS1; FOS1; SERA, EX2; HOA2; MAX, MOI; MC; MAFE; MAFF; MAFG; MEF2A; MF2; NF221; MF21; MF21; SEBF2; XRCC4; ZM21; ZW274 (inferredBy_MotifSimilarity), BACH1; BACH2; FOS; FOSB; FOS1; FOS1; FOS1; MotifSimilarity), BACH1; BACH2; FOS; FOSB; FOS1; FOS1; ME32; MATE; MAFE; MAFF; MAFG; MEF2A; MF2; NF221; MF21; MF21; SEBF2; MOtifSimilarity), HCX82; MF52; H574 (inferredBy_MotifSimilarity), FOX4; TNR32; H574 (inferredBy_MotifSimilarity), FOX4; TNR32; H574; InferredBy_MotifSimilarity), FOX4; TNR32; H574; InferredBy_MotifSimilarity), FOX4; FOX3; FOX3; FOX4; FOX4; FOX1; FOX2; FOX3; FOX1; FOX2; FOX3; FOX1; FOX2; FOX1; FOX4; FOX3; FOX3; FOX4; FOX4; FOX4; FOX1; FOX2; FOX3; FOX1; FOX2; FOX1; FOX2; FOX4; FOX1; FOX4; FOX3; FOX3; FOX4; FOX4; FOX4; FOX3; FOX1; FOX2; FOX3; FOX1; FOX1; FOX1; FOX1; FOX1; FOX1; FOX1; FOX1; FOX3; FOX1; FOX1; FOX1; FOX1; FOX3; FOX1;	3.23 3.19 3.19 3.19 3.17 3.17 3.17 3.17 3.17 3.16 3.15 3.15 3.15 3.15 3.15 3.15 3.15 3.12 3.09 3.09 3.08 3.08 3.08 3.08 3.08
tapide_tpids_HOX2_SOIS_ACAAVKSNNNNNNTACTA_CAP_repr factorbook_HPS1 citbg_M2251 hocomoco_ANDR_MOUSE.H11M0.0 A tapide_RR_DB0_RROWGSNNTGTVCY dbcordb_DR0_RROWGNNNTGTVCY dbcordb_DR0_RROWGNNTGTVCY dbcordb_DR0_RROWGNNTGTVCY hdpl_PSMA6 japar_MA0591.1 prefermnrMk0H1986 tranifsr_pro_M07100 dbcordb_B02166 tranifsr_pro_M0715 tranifsr_pro_M06871 tranifsr_pro_M06871 tranifsr_pro_M06898 citbg_M0715 tranifsr_pro_M06891 tranifsr_pro_M06891 tranifsr_pro_M06891 tranifsr_pro_M06891	HOX82; SOX15 (directAnnotation). HSF1 (directAnnotation). AR (inferredBy_Orthology). AR (directAnnotation). PSMA6 (directAnnotation). PSMA6 (directAnnotation). MAFK (inferredBy_Orthology). HSF1 (directAnnotation). NR3C1 (directAnnotation). POX71 (directAnnotation). POX84 (directAnnotation). POX84 (directAnnotation). POX84 (directAnnotation). POX84 (directAnnotation). POX84 (directAnnotation). POX84 (directAnnotation). POX84 (directAnnotation). POX84 (directAnnotation). POX824 (directAnnotation). POX824 (directAnnotation). NR3C1 (directAnnotation). NR3C1 (directAnnotation). NR3C1 (directAnnotation). NR3C1 (directAnnotation). NR3C1 (directAnnotation). NR3C1 (directAnnotation).	HCK82; H52; H54 (inferredBy_MottSimilarity). ME72A, IME21; CharleredBy_MottSimilarity). ME72A, IME21; CharleredBy_MottSimilarity). ME73A, IME21; CharleredBy_MottSimilarity). BRF1; CB82; CH62; CH62; CF64; CF644; CF644; CF644; CF64;	3.23 3.19 3.19 3.19 3.17 3.17 3.17 3.17 3.17 3.17 3.17 3.17
tapiet_plats_HOX2_SOI3_ACAAWSINNINMATIA_CAP_repr tapiet_plats_HOX2_SII3_ACAAWSINNINMATIA_CAP_repr citbp_CAP_repr tapiet_AR_DED_REWISE HILMO.0.A tapiet_AR_DBD_REWISE HILMO.0.A tapiet_PSMA6 tapiet_DSMAGE tapiet_DSMAGE <td>HOX82; SOX15 (directAnnotation). HST2 (directAnnotation). AR (inferredBy_Orthology). AR (directAnnotation). PSMA6 (directAnnotation). PSMA6 (directAnnotation). MAFK (inferredBy_Orthology). HST1 (directAnnotation). NBRC1 (directAnnotation). PAX6 (directAnnotation). PAX6 (directAnnotation). PAX6 (directAnnotation). PAX6 (directAnnotation). POX71 (directAnnotation). POX71 (directAnnotation). POX71 (directAnnotation). POX821 (directAnnotation). POX821 (directAnnotation). POX824 (directAnnotation). POX824 (directAnnotation). NR3C1 (inferredBy_Orthology). NF8212 (directAnnotation). POU272 (inferredBy_Orthology).</td> <td>HCX82; H572; H574 (InferredBy_MotISImiliarity), ME72A, ME72 (InferredBy_MotISImiliarity), CXX1, M821; M422; P68 (InferredBy_MotISImiliarity), M6123; M822; M612; P68 (InferredBy_MotISImiliarity), M6124; M822; M612; M612; M6124; M6124; M6124; M612; M612; M612; M612; M612; M612; M612; M612;</td> <td>3.23 3.19 3.19 3.19 3.17 3.17 3.17 3.17 3.17 3.17 3.17 3.17</td>	HOX82; SOX15 (directAnnotation). HST2 (directAnnotation). AR (inferredBy_Orthology). AR (directAnnotation). PSMA6 (directAnnotation). PSMA6 (directAnnotation). MAFK (inferredBy_Orthology). HST1 (directAnnotation). NBRC1 (directAnnotation). PAX6 (directAnnotation). PAX6 (directAnnotation). PAX6 (directAnnotation). PAX6 (directAnnotation). POX71 (directAnnotation). POX71 (directAnnotation). POX71 (directAnnotation). POX821 (directAnnotation). POX821 (directAnnotation). POX824 (directAnnotation). POX824 (directAnnotation). NR3C1 (inferredBy_Orthology). NF8212 (directAnnotation). POU272 (inferredBy_Orthology).	HCX82; H572; H574 (InferredBy_MotISImiliarity), ME72A, ME72 (InferredBy_MotISImiliarity), CXX1, M821; M422; P68 (InferredBy_MotISImiliarity), M6123; M822; M612; P68 (InferredBy_MotISImiliarity), M6124; M822; M612; M612; M6124; M6124; M6124; M612; M612; M612; M612; M612; M612; M612;	3.23 3.19 3.19 3.19 3.17 3.17 3.17 3.17 3.17 3.17 3.17 3.17
tapistHOX2_SOI3_ACAAWSINNINMATIA_CAP_repr tapistIDAX2_JOX2_SOI3_ACAAWSINNINMATIA_CAP_repr cibbpM2251 hccomocANDR_MOUSE H11M0.0.A tapateAR_DBD_RRGWACANINTGTVCY dbcordbDLAR_2F1_ENCSR000EVM_1_m1 dbcordbDLAR_2F1_ENCSR000EVM_1_m1 dbcordbDLAR_2F1_ENCSR000EVM_1_m12 hdpiPSMA6 JapatM0591.1 memAGALAR_ENCSR000EWL_1_m1 hdpiPSMA6 tanals_prM05916 transle_prM05126 transle_prM05126 transle_prM0513 hccomcosEX6_HUMAN H11M0.0.C hccomcosPX6_HUMAN H11M0.0.D dbcordbP0182A_ENCSR000ALH_1_m1 cibbM0747 transle_proM06871 cibbM6360 ttainsle_pro_M06871 taipsteD0126 ttaipsteD0127_DBD_INVTRMATATKYAWN thjale_P0127_DBD_INVTRMATATKYAWN thjale_T0-0128_DBD_SINVTRMATATKYAWN	HOX82, SOX15 (directAnnotation), HST2 (directAnnotation), AR (inferredBy_Orthology), AR (directAnnotation), PSMA6 (directAnnotation), PSMA6 (directAnnotation), MAFK (inferredBy_Orthology), HST2 (directAnnotation), FOX71 (directAnnotation), PAX6 (directAnnotation), PAX6 (directAnnotation), PAX6 (directAnnotation), PAX6 (directAnnotation), POLR2A (directAnnotation), POLR2A (directAnnotation), POLR2A (directAnnotation), POLR2A (directAnnotation), POLR2A (directAnnotation), POLR2A (directAnnotation), NR3C1 (dir	HCX82; H52; H54 (inferredBy_MotifSimilarity), ME72A, ME72 (inferredBy_MotifSimilarity), ME72A, ME72 (inferredBy_MotifSimilarity), ME73A, ME72 (inferredBy_MotifSimilarity), ME73A, ME72 (inferredBy_MotifSimilarity), ME74, ME74, ME74, ME74, SERF1; SEEF2; MCC4; ZME74, ME74, ME74, ME74, ME74, ME74, ME74, ME74, ME74, SERF1; SEEF2; MCC4; ZME74, ZME74, ME74, ME74, ME74, ME74, ME74, ME74, ME74, SERF1; SEEF2; MCC4; ZME74, ME74, ME75, ME74, ME74, ME74, ME74, ME74, ME74, SERF1; SEEF2; MCC4; ZME74, ME75, ME75, ME74, ME74, ME74, ME74, ME74, ME74, ME74, ME74, ME74, ME75, ME72, ME72, MF221, MF212, ME7213; SMMCC2 (inferredBy_MotifSimilarity), MCK21; MS22; H574 (inferredBy_MotifSimilarity), MCK21; MS22; H574 (inferredBy_MotifSimilarity), MCK21; MS22; MS74 (inferredBy_MotifSimilarity), MCK21; MS22; MS74 (inferredBy_MotifSimilarity), MCK21; MS22; MS74 (inferredBy_MotifSimilarity), GF726, GF721; TA71; TB9 (inferredBy_MotifSimilarity), GF726, GF721; TA74; TG701; FC702; FC702; FC703; FC703; FC703; FC703; FC7041; FC70	3.23 3.19 3.19 3.19 3.17 3.17 3.17 3.17 3.17 3.17 3.17 3.17
Lapide_It_pairs_HOX2_SOI3_ACAAWSISNNINMATTA_CAP_repr Lapide_It_pairs_HOX2_SOI3_ACAAWSISNNINMATTA_CAP_repr Latorbook_HS1 tabpide_RAP_DB0_RRAUSE H11M0.0 A Lapide_RAP_DB0_RRAWSISNITCIVCY dbcordb_PCI2A_ENCSR0000FW1_m1 dbcordb_PCI2A_ENCSR0000FW1_m1 hdpl_PSMA6 lapar_MAX0591.1 prefermnMAUT1806 transfs_rpm_M07100 dbcordb_R02166 transfs_rpm_M0710 dbcordb_PCI2A_ENCSR000AHL3_m1 home_ACAACASUCTGTCTT_ARE transfs_rpm_M05216 transfs_rpm_M0	HOX82; SOX15 (directAnnotation). HST2 (directAnnotation). AR (inferredBy_Orthology). AR (directAnnotation). PSMA6 (directAnnotation). PSMA6 (directAnnotation). MAFK (inferredBy_Orthology). HST2 (directAnnotation). RSC1 (directAnnotation). POXR2 (directAnnotation). PCXF1 (directAnnotation).	HCK82; H52; H54 (inferredBy_MottSimilarity). ME22, ME22 (inferredBy_MottSimilarity). ME23, ME22 (inferredBy_MottSimilarity). ME24, ME22 (inferredBy_MottSimilarity). ME25, ME22 (inferredBy_MottSimilarity). ME25, ME22 (inferredBy_MottSimilarity). ME21; ME22 (inferredBy_MottSimilarity). ME21; ME22 (inferredBy_MottSimilarity). BACH1; MACH2; FOS; FOSB; FOS1; FOS1; SKR4; ZH2; HOA2; MAX; MO1; MC; NLFE; NRF1; POLR24; MA22; IN895; SKR4; SKR4; SKR4; ZH2; HOA2; MAX; MO1; MC; NLFE; NRF1; POLR24; MA22; IN895; SKR4; SKR4; SKR4; ZH2; HOA2; MAX; MO1; MC; NLFE; NRF1; POLR24; MA22; IN895; SKR4; SKR4; SKR4; SKR4; ZH2; HOA2; MAX; MO1; MC; MAF; MAFG; ME724; INF2; NF24; INF24; SKR4; SKR4; SKR4; SKR4; MAX; MARE; MAFG; ME724; NF2; NF24; INF24; SKR4; SKR4; MAX; SKR4; MAX; MAX; MARE; MAFG; ME724; NF2; NF24; INF24; SKR4; MAX; SKR4; MAX; SKR4; MAX; MARE; MAFG; ME724; NF2; NF24; INF24; INF24; SKR4; MAX; SKR4; MAX; MAX; MARE; MAFG; ME724; NF2; NF24; INF24; INF24; SKR4; MAX; SKR4; MAX; MAX; MARE; MAFG; ME724; NF2; NF24; INF24; INF24; SKR4; MAX; SKR4; MAX; MAX; MARE; MAFG; ME724; NF2; NF24; INF24; INF24; SKR4; MAX; SKR4; MAX; MAX; MARE; MAFG; ME724; NF2; NF24; INF24; INF24; SKR4; MAX; SKR4; INF34; INF34; FOXA; FOXA; FOXA; FOXA; FOXA; MAX; SKR4; FOXA; F	3.23 3.19 3.19 3.19 3.17 3.17 3.17 3.17 3.17 3.17 3.17 3.17
tapiet_plats_HOX2_SOI3_ACAAWSINNINMATIA_CAP_repr tapiet_plats_HOX2_SII3_ACAAWSINNINMATIA_CAP_repr citbp_LAPSI tapiet_AR_DED_REWOUSE HILMO.0.A tapiet_AR_DBD_REWOUSE HILMO.0.A tapiet_AR_DBD_REWOUSE HILMO.0.A tapiet_AR_DBD_REWOUSE HILMO.0.A tapiet_AR_DBD_REWOUSE HILMO.0.A tapiet_AR_DBD_REWOUSE HILMO.0.A tapiet_AR_DBD_REWOUSE HILMO.0.A tapiet_Plats_DBD_REWOUSE HILMO.0.A tapiet_Plats_DBD_REWOUSE HILMO.0.A tapiet_Plats_DBD_REWOUSE HILMO.0.A tapietminite_DEVENDENT_INFORMET_INFORMET hdpi_PSMA6 tapietminite_DEVENDENT_ARE tapietminite_DEVENDENT_ARE tapietminite_DEVENDENT_ARE tapietminite_pro_MORS73 hocomodeEX3_HUMAN HILMO.0.D decordb_POLR2A_ENCROROALH_1_m1 citbp_M0747 tapietminite_pro_M06871 tapietminite_pro_M06898 citbp_M0715 tapiet_pol22_DBD_NWTEMATATX/WIN fylectorsurveyD198_F10-12_SANGER_5_FBeg0022699 tapiet_FOXD 200_DED ETAAVA	HOX82; SOX15 (directAnnotation). HST2 (directAnnotation). AR (inferredBy_Orthology). AR (directAnnotation). PDXRA (inferredBy_Orthology). HST2 (directAnnotation). MAFK (inferredBy_Orthology). HST2 (directAnnotation). RSS1 (directAnnotation). PDXB2 (directAnnotation).	HCX82; H52; H54 (Inferredby, MottSimilarity), ME2A, ME22 (Inferredby, MottSimilarity), CXA1, M821; M822; P64 (Inferredby, MottSimilarity), ME12A, ME22 (Inferredby, MottSimilarity), ME12A, M822; M825; M824; P64; M844; M845;	3.23 3.19 3.19 3.19 3.17 3.17 3.17 3.16 3.16 3.16 3.15 3.15 3.14 3.13 3.12 3.09 3.09 3.09 3.08 3.08 3.08 3.07 3.07 3.07 3.06
tapale_tpains_HOX2_SOI3_ACAAWSISNNINMATIA_CAP_repr factorbook_HP31 citbg_M2251 hccomoc_ANDR_MOUSE H11M0.0.A tapale_AR_DBD_RRSWACANNINTGTVCY decordb_HAC2F1_ENCSR000EVM_1_m1 decordb_D202A_DESCR000BVL_1_m1 hdpi_PSMA6 Hspar_MAD511 hdpi_PSMA6 Hspar_MAD511 hccomoc_PXA2_NESCR000BHE_1_m1 hccomoc_PXA2_HOX300BHE_1_m1 hccomoc_PXA2_HUMAH11M0.0.C hccomoc_PXA2_HUMAH11M0.0.D decordb_P0LR2A_ENCSR000AH1_m1 cibg_M0747 transfac_pro_M06871 tapale_POL22_BD_NWTRMATATRYAWN tipale_POL22_BD_NTRMATATRYAWN tipale_POL22_BD_NTRMATATRYAWN tipale_POL22_BD_NTAMAYA	HXX82;SXX15 (directAnnotation), HXF1 (directAnnotation), AR (inferredBy_Orthology), AR (directAnnotation), PSMA6 (directAnnotation), PSMA6 (directAnnotation), MAFK (inferredBy_Orthology), HSF1 (directAnnotation), PAX8 (directAnnotation), PXX8 (directAnnotation), PXX82 (directAnnotation), PXX82 (directAnnotation), PXX824 (directAnnotation), PXX824 (directAnnotation), PXX824 (directAnnotation), PXX824 (directAnnotation), PXX824 (directAnnotation), PXX823 (prectAnnotation), PXX824 (directAnnotation), PXX823 (directAnnotation), PXX823 (directAnnotation), PXX823 (directAnnotation), PXX823 (directAnnotation), PXX823 (directAnnotation), PXX824 (directAnnotation), PXX84 (directAn	HCX82; H52; H54 (InferredBy_MotISImiliarity). ME72A, ME72 (InferredBy_MotISImiliarity). ME72A, ME72 (InferredBy_MotISImiliarity). ME73A, ME72 (InferredBy_MotISImiliarity). ME74A, ME72, INS2, ICC, P26, P56, P58A, C292, HCA2, MAY, MOTI, MCC, NELFE, NBF1, POLR2A, M2021; B895; C4881; CTCF; E264; C58A, C292, HCA2, MAY, MOTI, MCC, NELFE, NBF1, POLR2A, M2021; B895; C4884; CTCF; E264; C58A, C292, HCA2, MAY, MOTI, MCC, NELFE, NBF1, POLR2A, M2021; B895; C4884; CTCF; E264; C58A, C292, HCA2, MAY, MOTI, MCC, NELFE, NBF1, POLR2A, M2021; B895; C4834; CTCF; E264; C58A, C292, HCA2, MAY, MOTI, MCC, NELFE, NBF1, POLR2A, M2021; B895; C484; MAY, S18B1; S18B2; XHCC4; ZMI21; ZM274 (InferredBy_MotISImiliarity). BCH1; BCH2; FC5; FO58; FO51; FC51; JCN2; JUN8; JUN9; JUN9; MAF5; MAF6; MAF6; M6F2A, M722; MF221; MF212; MF212; SMARCC2 (InferredBy_MotISImiliarity). HCX82; H572; H574 (InferredBy_MotISImiliarity). FCXA1; M32; FC61 (InferredBy_MotISImiliarity). FCXA1; M33; FC81 (InferredBy_MotISImiliarity). FCXA1; FC81; FC81; InferredBy_MotISImiliarity). FCXA1; FC801; FC804; InferredBy_MotISImiliarity). FCXA1; FC801; FC804; FC804; ICC82; FC802; FC802; FC802; FC802; FC801; FC8041; FC8041; FC804; FC804; FC804; FC804; ICC82; FC802; FC802; FC802; FC802; FC802; FC804; FC8041; FC804; FC804; FC804; FC804; FC804; FC804; FC804; FC804; FC804; FC8041; FC804; FC804; FC804; FC804; FC804; FC804; FC804; FC804; FC804; FC804; FC804]; FC804; FC804; FC804; FC804; FC804; FC804; FC804; FC804; FC804; FC804; FC804]; FC804; FC804; FC804]; FC804; FC804; FC804	3.23 3.19 3.19 3.19 3.17 3.17 3.16 3.17 3.16 3.15 3.15 3.15 3.15 3.15 3.15 3.14 3.13 3.12 3.09 3.09 3.09 3.09 3.09 3.09 3.09 3.00 3.00
tapide_tpids_tPIX2_SOIS_ACAAWSISNNNNATA_CTA_CAP_repr tatiothooL_HS1 citbg_M2351 hccomoc_JANDR_MOUSE_H11MO.0.A tapide_AR_DB0_RROWGENTIMO.0.A tapide_AR_DB0_RROWGENTIMO.0.A tapide_AR_DB0_RROWGENTIMO.0.A tapide_AR_DB0_RROWGENTIMO.0.A tapide_AR_DB0_RROWGENTIMO.0.A tapide_TAR_DB0_RROWGENTIMO.0.A tapide_TAR_DB0_RROWGENTIMO.0.C hccomoco_LKAS_HUMAN H11MO.0.C hccomoco_LKAS_HUMAN H11MO.0.C hccomoco	HOX82; SOX15 (directAnnotation). HST2 (directAnnotation). AR (inferredBy_Orthology). AR (inferredBy_Orthology). HST2 (directAnnotation). PSMA6 (directAnnotation). MAFK (inferredBy_Orthology). HST2 (directAnnotation). RSC1 (directAnnotation). POXR24 (directAnnotation). PCXF1 (directAnnotation). PCXF2 (di	HCK82; H52; H54 (inferredBy_MotifSimilarity). HCK82; H52; H54 (inferredBy_MotifSimilarity). HCK82; H52; H54 (inferredBy_MotifSimilarity). HCK81; H82; L0R2; CR82; PCB, H54; M54; M451; H572; H574 (inferredBy_MotifSimilarity). B87; L0R2; H832; L0R2; H54; H54; H54; H54; H54; H572; H574 (inferredBy_MotifSimilarity). B87; L0R2; H832; L0R4; H54; H54; H54; H54; H54; H572; H574 (inferredBy_MotifSimilarity). B67; L0R2; H552; H54; InferredBy_MotifSimilarity). B67; L18; H52; H54; InferredBy_MotifSimilarity). B67; L18; H52; H54; InferredBy_MotifSimilarity). B67; L18; H52; H54; InferredBy_MotifSimilarity). B67; L18; H52; H54; InferredBy_MotifSimilarity). B7; L14; H54; H54; H54; InferredBy_MotifSimilarity). F0; L1; H54; H56; F0; H1; H56; H56; H56; H56; H56; H56; H56; H56	3.23 3.19 3.19 3.19 3.17 3.17 3.17 3.17 3.16 3.16 3.16 3.15 3.15 3.15 3.15 3.15 3.15 3.15 3.15
LipJiel, L. JOX2, 2003, ACAAWSINNINMATIA, CAP, repr LipJiel, L. JOX2, 2013, ACAAWSINNINMATIA, CAP, repr Libtorbook, JPSJ. LipJiel, AR, DBD, RROUSE HI 1MO, 0. A LipJiel, AR, DBD, RROWGH, MINTOTIVCY dbcordb_PLACEF1_ENCSR000EVM_1_m1 dbcordb_PLACEF1_ENCSR00DOLVM_1_m12 hdpl_PSMA6 lipp_MM0591.1 preferen_mMotIf386 transfer_pro_M07100 dbcordb_PO2166 transfer_pro_M07216 transfer_pro_M07373 hocomoco_EXAS_HUMAN HI 1MO 0. C hocomoco_EXAS_HUMAN HI 1MO 0. C dbcordb_PO2165 transfer_pro_M08918 cisbp_M0715 transfer_pro_M08918 cisbp_M0715 transfer_pro_M08918 cisbp_M0715 transfer_pro_M08918 cisbp_M0715 transfer_pro_200366 tipale_F0x02_DBD_NWTRMATATX/WNN Mp4ctorsurvey_D198_F10-12_SANGER_5_F8p00022699 tipale_F0x02_DBD_RTAAV/A transfer_pro_M00641	HOX82; SOX15 (directAnnotation). HST2 (directAnnotation). AR (inferredBy_Orthology). AR (directAnnotation). PSMAG (directAnnotation). PSMAG (directAnnotation). MAFK (inferredBy_Orthology). HST2 (directAnnotation). EXS12 (directAnnotation). EXS12 (directAnnotation). EXS12 (directAnnotation). PAK6 (directAnnotation). EXS12 (directAnnotation). POLR2A (directAnnotation).	HCX82; H52; H54 (InferredBy_MotISImilarity), ME2A, ME22 (InferredBy_MotISImilarity), CXA1, M821; M822; P68 (InferredBy_MotISImilarity), M821; M822; M822; P68 (InferredBy_MotISImilarity), M821; M822; M822; M822; P68 (InferredBy_MotISImilarity), M821; M822; M822; M822; M822; M822; M822; M822; M822; M821; M821; M822; M822; M822; M882; M822; M823; M822; M823; M8	3.23 3.19 3.19 3.19 3.17 3.17 3.17 3.17 3.16 3.16 3.16 3.16 3.16 3.15 3.15 3.15 3.13 3.12 3.09 3.09 3.09 3.09 3.00 3.00 3.00 3.00
tapide_tpids_HOX2_SOIS_ACAAWSISNNINMATIA_CAP_repr factobooL_HP31 citbg_M2251 hccomoc_ANDR_MOUSE H11M0.0.A tapide_AR_DB0_RRSWACANNINTGTVCY decordb_HA-E2F1_ENCSR000EVM_1_m1 decordb_P012_ALSCSR002A00_1_m12 hdpi_PSMA6 Hspar_MAD551.1 prefermnfwA0551.2 Hspar_M0555.2 Hspar_M0555.2 Hs	HOX82, SOX15 (directAnnotation), HST2 (directAnnotation), AR (inferredBy_Orthology), AR (directAnnotation), POXRA (inferredBy_Orthology). HST2 (directAnnotation), MAFK (inferredBy_Orthology). HST2 (directAnnotation), PAX8 (directAnnotation), PAX8 (directAnnotation), PAX8 (directAnnotation), POXR1 (directAnnotation), POXR1 (directAnnotation), POXR2 (directAnnotation), POXR2 (directAnnotation), POXR2 (directAnnotation), POXR2 (directAnnotation), POXR2 (directAnnotation), POXR2 (directAnnotation), NFRC1; SP11 (directAnnotation), NFRC1; SP11 (directAnnotation), NFRC1; SP11 (directAnnotation), NFRC1; SP11 (directAnnotation), NFRC1; SP11 (directAnnotation), NFRC1; SP11 (directAnnotation), NFRC1; (directAnnotation), HSF2 (directAnnotation), HSF2 (directAnnotation), HSF2 (directAnnotation), HSF2 (directAnnotation), HSF2 (directAnnotation), NFRC1; (directAnnotation), HSF2 (directAnnotation), HSF2 (directAnnotation), HSF2 (directAnnotation), HSF2 (directAnnotation), HSF2 (directAnnotation), NF212 (directAnnotation),	HCX82; H52; H54 (InferredBy_MotISImiliarity). ME2A, ME22 (InferredBy_MotISImiliarity), ME2A, ME22 (InferredBy_MotISImiliarity), ME2A, ME22 (InferredBy_MotISImiliarity), ME3C, ME22 (InferredBy_MotISImiliarity), ME3C, ME22 (InferredBy_MotISImiliarity), ME3C, ME22 (InferredBy_MotISImiliarity), ME4C, ME4C, M	3.23 3.19 3.19 3.19 3.17 3.17 3.17 3.16 3.16 3.16 3.15 3.15 3.14 3.13 3.13 3.12 3.12 3.12 3.12 3.12 3.09 3.09 3.09 3.08 3.08 3.08 3.07 3.07 3.07 3.07 3.05 3.05 3.05 3.04 3.04
Lapide_It_pairs_HOX2_SOI3_ACAAWSISNNINMATIA_CAP_repr Lapide_It_pairs_HOX2_SOI3_ACAAWSISNNINMATIA_CAP_repr Latorbook_HS1 Labobac_APL_0X2511 hccomcoc_ANDR_MOUSE.H11MO.0.A Lapide_AR_DB0_RROWACANNINTCIVCYY decordb_PLA22F1_ENCSR00004U1_m1 decordb_PLA22F1_ENCSR00004U1_m12 hdpl_PSMA6 lipapr_MA05511 preferm_InMAUTI986 transfs_pro_M07100 decordb_PLA22_ENCSR0004H1_m1 home_AGAACASIXCTGTCTT_ARE transfs_pro_M07206 transfs_pro_M07373 hccomcoc_ELK3_HUMAN.H11MO.0.C hccomcoc_ELK3_HUMAN.H11MO.0.C hccomcoc_ELK3_HUMAN.H11MO.0.C hccomcoc_ELK3_HUMAN.H11MO.0.C hccomcoc_ELK3_HUMAN.H11MO.0.C hccomcoc_ELK3_HUMAN.H11MO.0.C hccomcoc_ELK3_HUMAN.H11MO.0.C hccomcoc_ELK3_HUMAN.H11MO.0.C hccomcoc_ELK3_HUMAN.H11MO.0.C hccomcoc_ELK3_HUMAN.H11MO.0.C hccomcoc_ELK3_HUMAN.H11MO.0.C hccomcoc_ELK3_HUMAN.H11MO.0.C hccomcol_ELK3_HUMAN.H11MO	HOX82; SOX15 (directAnnotation), HST2 (directAnnotation), AR (inferredBy_Orthology), AR (inferredBy_Orthology), HST2 (directAnnotation), PSMA6 (directAnnotation), MAFK (inferredBy_Orthology). HST2 (directAnnotation), AR3C1 (directAnnotation), PSX6 (directAnnotation), PSX6 (directAnnotation), PSX6 (directAnnotation), PSX6 (directAnnotation), PSX6 (directAnnotation), PSX6 (directAnnotation), PSX6 (directAnnotation), POR224 (directAnnotation), POR224 (directAnnotation), POR224 (directAnnotation), POR224 (directAnnotation), POR224 (directAnnotation), POU222 (inferredBy_Orthology), POU222 (inferredBy_Orthology), POU222 (inferredBy_Orthology), NFE12 (directAnnotation), HST2 (directAnnotation),	HCK82; H52; H54 (inferredBy_MotISimilarity). HCK82; H52; H54 (inferredBy_MotISimilarity). HCK82; H52; H54 (inferredBy_MotISimilarity). HCK81; H82; L612; HCR2; P66 (inferredBy_MotISimilarity). HS12; H82; H52; H54; HCK2; P66 (inferredBy_MotISimilarity). HS12; H83; H52; H54; HCK2; H54; H54; H54; H54; H54; H54; H54; H54	3.23 3.19 3.19 3.17 3.17 3.17 3.17 3.16 3.15 3.15 3.15 3.15 3.15 3.14 3.14 3.13 3.12 3.09 3.09 3.09 3.09 3.09 3.00 3.00 3.00
tapale_fl_pairs_HOXE2_SOIS_ACAAVKENNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN	HOX82; SOX15 (directAnnotation), HST2 (directAnnotation), AR (inferredBy_Orthology), AR (directAnnotation), PSMA6 (directAnnotation), PSMA6 (directAnnotation), MAFK (inferredBy_Orthology), HST2 (directAnnotation), RS21 (directAnnotation), PSMA6 (directAnnotation), PSMA6 (directAnnotation), POR2A (directAnnotation), POR2A (directAnnotation), POR2A (directAnnotation), POR2A (directAnnotation), POR2A (directAnnotation), POR2A (directAnnotation), POR2A (directAnnotation), POR2A (directAnnotation), POR2A (directAnnotation), POL2A (directAnnotation), POLAA (directAnnotation), POLAA (directAnnotation), POLAA (directAnnotation), POLAA (directAnnotation), POLAA (direct	HCX82; H52; H54 (inferredby, MottSimilarity), ME2A, ME22 (inferredby, MottSimilarity), ME2A, ME22 (inferredby, MottSimilarity), ME3C, ME32 (inferredby, MottSimi	3.23 3.19 3.19 3.19 3.17 3.17 3.17 3.17 3.17 3.17 3.17 3.17
tapiet_plats_JOX2_SOI3_ACAAVISINNINMATIA_CAP_repr tapiet_plats_JOX2_SOI3_ACAAVISINNINMATIA_CAP_repr citbg_LAP_2SI1 hccomocoANDR_MOUSE H11MO.0.A tapiet_AR_DBD_RRSWACANINTGTVCY decordb_UAX251 hccincol_MOR_MOUSE H11MO.0.A tapiet_AR_DBD_RRSWACANINTGTVCY decordb_UAX271_ENCR000EVM_1_m1 hdpi_PSMA6 tapiet_prc_MO05101 predmmmKM0017866 transfe_prc_M00216 transfe_prc_M00216 transfe_prc_M00216 transfe_prc_M00216 transfe_prc_M00216 transfe_prc_M00216 transfe_prc_M00871 cibp_M0747 transfe_prc_M06871 cibp_M0715 transfe_prc_M06871 transfe_prc_M06871 tapiet_P0122_DBD_NVTEMATATXVWN Mpdietorsurvey_D198_F1012_SANGER_5_F8p0022699 tapiet_P0126_DBD_RTAAVA transfe_prc_M00831 transfe_prc_M00261 cibg_M0603 transfe_prc_M00386 transfe_prc_M00386 transfe_prc_M00386	HOX82, SOX15 (directAnnotation), HST2 (directAnnotation), AR (inferredBy_Orthology), AR (directAnnotation), POXRA (inferredBy_Orthology). HST2 (directAnnotation), NR3C1 (directAnnotation), PAKE (inferredBy_Orthology). EXE3 (directAnnotation), POXR1 (directAnnotation), POXR1 (directAnnotation), POXR1 (directAnnotation), POXR2 (di	HCX82; H572; H574 (InferredBy_MotISImiliarity), ME22, ME22; (InferredBy_MotISImiliarity), ME23, ME22; (InferredBy_MotISImiliarity), ME32, ME32; (InferredBy_MotISImiliarity), ME32; ME32; (InferredBy_MotISImiliarity), ME32; ME32; (InferredBy_MotISImiliarity), ME32; ME32; (InferredBy_MotISImiliarity), ME32; ME32; ME32; ME32; ME32; ME32; ME32; ME32; ME32; ME32; ME32; InferredBy_MotISImiliarity, ME32; ME32; ME32; ME32; ME32; ME32; ME32; ME32; ME32; ME32; ME32; ME	3.23 3.19 3.19 3.19 3.17 3.17 3.17 3.17 3.17 3.17 3.17 3.17
Lapide_It_pairs_HOX2_SOI3_ACAAVKSNNNNNATIA_CAP_repr Lapide_IT_pairs_HOX2_SOI3_ACAAVKSNNNNNATIA_CAP_repr Latorbook_HS1 Laboback_IS1 Laboback_IS1 Accomba	HOX82; SOX15 (directAnnotation). HST2 (directAnnotation). AR (inferredBy_Orthology). AR (inferredBy_Orthology). HST2 (directAnnotation). PSMA6 (directAnnotation). NA87L (inferredBy_Orthology). HST2 (directAnnotation). POX72 (directAnnotation). POX82 (directAnnotation). POU282 (directAnnotation). NFATC3; SP11 (directAnnotation). HST3 (directAnnotation). HST3 (directAnnotation). POU282 (inferredBy_Orthology). NFE12 (directAnnotation). HST3 (directAnnotation). HST3 (directAnnotation). SOX10 (inferredBy_Orthology). NFE12 (directAnnotation). HST3 (directAnnotation).	HCK82; H52; H54 (InferredBy_MotISImilarity). HCK82; H52; H54 (InferredBy_MotISImilarity). HCK82; H52; H54 (InferredBy_MotISImilarity). HCK81; H82; L612; HCR2; P68 (InferredBy_MotISImilarity). HCK81; H82; L612; HCR2; HCK8; H58A; E242; HOA2; MAX; M01; MCY, NLFE; NBF1; POLR2; HCK82; H582; H545 (InferredBy_MotISImilarity). BF1; L58P; C68B; ICCF; F26; L58A; E242; HOA2; MAX; M01; MCY, NLFE; NBF1; POLR2; HCK82; H552; H545 (InferredBy_MotISImilarity). BACH1; BACH2; F05; F05B; F051; F051; J101; J101; J101; J101; MCF; MAFE; MAFE; MAFE; MAFE; MF2; HF2; NF2L; NF2L2; NF2L2; SMARC2 (InferredBy_MotISImilarity). BACH1; BACH2; F05; F05B; F051; F051; J101; J001; J1001; J101; J1	3.23 3.19 3.19 3.17 3.17 3.17 3.17 3.17 3.17 3.17 3.17
tapiat_plais_HOX2_SOI3_ACAAVISINNINMATIA_CAP_repr tapiat_plais_HOX2_SOI3_ACAAVISINNINMATIA_CAP_repr tatorbook_HSI tapiat_AR_DBO_RROUSE H11MO.0.A tapiat_AR_DBO_RROWAGNINTGIVCY decordb_PLAE2F1_ENCSR0000EVM_1_m1 decordb_PLAE2F1_ENCSR000EVM_1_m1 hdpl_PSMA6 japar_MA0591.1 preferm_infw6U19366 transfs_rpr_M07100 decordb_PC0126 transfs_rpr_M07216 transfs_rpr_M0727 transfs_rpr_M0737 transfs_rpr_M089718 tapiate_rror_M08978 tapiate_rror_M08978 tapiate_rror_M08978 tapiate_rror_M08978 tapiate_rror_M08978 tapiate_rror_M08978 tapiate_rror_M08978 tapiate_rror_M08978 tapiate_rror_M08978 tapiate_rror_M08978 tapiate_rror_M08978 tapiate_rror_M08978 tapiate_rror_M08978 tapiate_rror_M08978 tapiate_rror_M08978 tapiate_rror_M07765 transfs_rror_M09388 tapiate_rror_M09388 tapiate_rror_M09388 tapiate_rror_M09388 tapiate_rror_M09388	HOX82; SOX15 (directAnnotation). HSF1 (directAnnotation). AR (inferredBy_Orthology). AR (directAnnotation). PSMA6 (directAnnotation). PSMA6 (directAnnotation). MAFK (inferredBy_Orthology). HSF1 (directAnnotation). PSMA6 (directAnnotation). PSMA6 (directAnnotation). PSMA6 (directAnnotation). POR2A (directAnnotation). POR2A (directAnnotation). POR2A (directAnnotation). POR2A (directAnnotation). POR2A (directAnnotation). POR2A (directAnnotation). POR2A (directAnnotation). POR2A (directAnnotation). POL2A (directAnnotation). POL2A (directAnnotation). POL2A (directAnnotation). POL2A (directAnnotation). POL22 (directAnnotation).	HCX82; H52; H54 (InferredBy_MotISImilarity), ME2A, ME22 (InferredBy_MotISImilarity), CXA1, M821; M822, CPR (InferredBy_MotISImilarity), M823, M822, M822, CPR (InferredBy_MotISImilarity), M821; M822, M822, CPR (InferredBy_MotISImilarity), M821; M822, M822, CPR (InferredBy_MotISImilarity), M821; M822, M822, CPR (InferredBy_MotISImilarity), M621; M822, M822, M824, StREP; SRRA; CPR, 2M22, MA2; M01; MYC, N81; F, N851; P028; M622, M823, M824, StREP; SRRA; CPR, 2M24, M01; MYC, N81; F, N851; P028; M622, M825, M824, StREP; SRRA; CPR, 2M24, M01; MYC, N81; F, N851; P028; M622, M825, M824, M645, StREP; SRRA; CPR, 2M24, M01; MYC, N81; F, N851; P028; M622, M825, M824, M645, StREP; SRRA; CPR, 2M24, M645, M475, M476, M475, M476, M477, M622, M825, M824, M645, M647, M645, M647, M645, M647, M476, M477, M627, M627, M647, M647, M645, M641, M645, M647, M647, M476, M477, M476, M477, M627, M647, M647, M647, M645, M641, M645, M647, M647, M476, M477, M476, M477, M647, M647, M647, M647, M641, M641, M641, M647, M647, M476, M477, M476, M477, M647, M647, M647, M647, M641, M641, M641, M641, M641, M647, M476, M477, M476, M477, M647, M647, M643, M641, M641, M641, M641, M641, M641, M647, M476, M477, M476, M647, M476, M477, M647, M647, M643, M643, M641, M641, M641, M641, M641, M641, M641, M647, M476, M647, M647, M647, M647, M647, M641, M647, M647, M641, M641, M641, M641, M641, M647, M641, M64	3.23 3.19 3.19 3.19 3.17 3.17 3.17 3.17 3.17 3.17 3.17 3.17
LipJiel, L. JOX2, 2003, ACAAVISINNINMATIA, CAP, repr LipJiel, L. JOX2, 2013, ACAAVISINNINMATIA, CAP, repr LipJiel, AR, DRD, RRUSE, H11MO, 0, A LipJiel, AR, DBD, RRUSE, M11MO, 0, A LipJiel, AR, DBD, RRUSE, M11MO, 0, A LipJiel, AR, DBD, RRUSE, LINCONDUL, 1, m1 McGordb, PURZA, ENSRODOAU, 1, m12 McGin, PS, MAG, SILL, LINCONDUL, 1, m1 homer, AGALASHCTGTCTT, ARE Linafda, pro_M00373 hocomoca, LIS, MUMAH H11MO, 0, C hocomoca, LIS, MUMAH H11MO, 0, D decordb, POUR2A, ENCRODOALH, 1, m1 clibp_M0715 Linafda, pro_M06871 Linafda, pro_M06871 LipJiel, POUR2A, ENCRODOALH, 1, m1 Midmer, MN00186 LipJiel, POUR2A, ENCRODOALH, 1, m1 Midmer, MN00186 LipJiel, POUR2A, ENCRODOALH, 1, m1 LipJiel, POUR2B, TOL2, S	HOX82; SOX15 (directAnnotation), HST2 (directAnnotation), AR (inferredBy_Orthology), AR (directAnnotation), POXRA (inferredBy_Orthology). HST2 (directAnnotation), MARK (inferredBy_Orthology). HST2 (directAnnotation), POXR2 (di	HCX82; H572; H574 (InferredBy_MottSimilarity), ME2A, ME272 (InferredBy_MottBimilarity), CXA1, M821; M822; P68, P68, MettSimilarity), M821; M822; M822; P68, P68, MettSimilarity), M821; M822; M822; M422; P68, P68, MettSimilarity), M821; M822; M822; M424; MettSimilarity), M821; M822; M822; M424; MettSimilarity), M821; M822; M822; M424; MettSimilarity), M422; M822; M424; MettSimilarity), M421; M424; M445; M444; MettSimilarity), M421; M424; M445; M444; M444; M444; M444; M446; M472; M446; M472; M446; M472; M446; M472; M446; M472; M446; M472; M446; M446; M446; M447; M446; M472; M446; M446; M446; M446; M447; M446; M472; M446; M446; M446; M447; M446; M472; M446; M446	3.23 3.19 3.19 3.19 3.17 3.17 3.17 3.17 3.17 3.17 3.17 3.17
Lapide_T_DATSTOXE_2ODIS_ACAAWSENNINMATTA_CAP_repr Lapide_T_DATSTOXE_2ODIS_ACAAWSENNINMATTA_CAP_repr Latorbook_IPS1 citbgM2251 hccomcco_ANDR_MOUSE.HI1MO.0.A Lapide_R_D_BOB_RROWACANINTCTIVCY decordb_TAR_EF1_ENCSR000EVM_1_m1 decordb_TAR_EF1_ENCSR000EVM_1_m12 hcpl_PSMA6 lipagr_MA0551.1 prefermInMAUTI986 transfs_prcM00516 transfs_prcM005216 transfs_prcM005216 transfs_prcM005216 transfs_prcM005216 transfs_prcM005216 transfs_prcM005216 transfs_prcM005216 transfs_prcM005216 transfs_prcM005216 transfs_prcM005216 transfs_prcM005216 transfs_prcM006871 cibgM0715 transfs_prcM006871 transfs_prcM006871 transfs_prcM006871 transfs_prcM006871 transfs_prcM006871 transfs_prcM00586 transfs_prcM00586 transfs_prcM00541 cibgM6053 transfs_prcM07265 hccomcrcSXID_M0USE.H11M0.1.A transfs_prcM0726 prefermM002164	HOX82; SOX15 (directAnnotation). HST2 (directAnnotation). AR (inferredBy_Orthology). AR (inferredBy_Orthology). HST2 (directAnnotation). POMAG (directAnnotation). HST2 (directAnnotation). POX82 (directAnnotation). POUR22	HCX82; H52; H54 (InferredBy_MottSimilarity). ME2A, ME22 (InferredBy_MottSimilarity). ME2A, ME22 (InferredBy_MottSimilarity). ME3C1; M822 (InferredBy_MottSimilarity). ME3C1; M822 (InferredBy_MottSimilarity). ME3C1; M822 (InferredBy_MottSimilarity). ME4C1; M822 (InferredBy_MottSimilarity). MCX2; M522; H524 (InferredBy_MottSimilarity). MCX4; M843; F64 (InferredBy_MottSimilarity). MCX4; M643; F64 (InferredBy_MottSimilarity). MCX4; M543; F64 (InferredBy_MottSimilarity). MCX4; M543; F64 (InferredBy_MottSimilarity). MCX4; M543; F64 (InferredBy_MottSimilarity). MCX4; M544; F64 (InferredBy_MottSimilarity). MCX4; M544; F64 (InferredBy_MottSimilarity). MCX4; M544; F64 (InferredBy_MottSimilarity). MCX4; M544; F64 (InferredBy_MottSimilarity). MCX4; MCX4; F64 (Inferre	3.23 3.19 3.19 3.17 3.17 3.17 3.17 3.17 3.17 3.17 3.17
tapide_tpins_H0x82_5013_ACAAVK5NNNNNNTATA_CAP_repr tatorbook_H931 citbg_M2351 hocomoco_ANDR_M0USE.H11MO.0.A tapide_AR_DB0_RROWAGNINTGTWCY dbcordb_DR0_RROWAGNINTGTWCY dbcordb_DR0_ST_ANSA00A041_m1 dbcordb_DR0_ST_ANSA00A041_m12 hdpl_PSMA6 japar_MA0591.1 prefermmNeU1986 tranifs_rpr_M07100 dbcordb_R0216 tranifs_rpr_M0710 dbcordb_DR0216 tranifs_pro_M08718 citbg_M0715 tranifs_pro_M08998 citbg_M0715 tranifs_pro_M08998 citbg_M0715 tapide_F0x2_DB_NVTRMATATXXWN frfctorsurve_D198_F10-12_SANGEK_5_FBp0022699 tapide_F0x226 tanifs_pro_M09318 citbg_M07265 tranifs_pro_M0938 citbg_M603 tapide_F0x2_DB_NVTRMATATXXWN frfctorsurve_D198_F10-12_SANGEK_5_FBp0022699 tapide_F0x226 tanifs_pro_M0938 citbg_M0726 tranifs_pro_M07265 hocomoco_SX10_M0USE.H11MO.1.A tranifs_pro_M0738 citbg_M0726 pro_M0726 tapide_F0x20_DB_NTRANAFA	HXX82;SXX15 (directAnnotation). HXF1 (directAnnotation). AR (inferredBy_Orthology). AR (inferredBy_Orthology). HXF2 (directAnnotation). PXMA6 (directAnnotation). MAFK (inferredBy_Orthology). HXF1 (directAnnotation). PXX16 (directAnnotation). PXX16 (directAnnotation). PXX6 (directAnnotation). PXX6 (directAnnotation). PXX82 (directAnnotation). NFE212 (directAnnotation). NFE212 (directAnnotation). NFE212 (directAnnotation). SXX10 (inferredBy_Orthology). NFE212 (directAnnotation). FXX10 (inferredBy_Orthology). NFE212 (directAnnotation). FXX10 (inferredBy_Orthology). NFE212 (directAnnotation). FXX10 (inferredBy_Orthology). NFE212 (directAnnotation). FXX10 (inferredBy_Orthology). NFE212 (directAnnotation). FXX10 (inferredBy_Orthology). NFE212 (directAnnotation). FXX10 (inferredBy_Orthology). NFE212 (directAnnotation). SX10 (inferredBy_Orthology). NFE212 (directAnnotation). SX10 (inferredBy_Orthology). NFE212 (directAnnotation).	HCK22; H52; H54 (inferredby_MottSimilarity), ME2A, ME22 (inferredby_MottSimilarity), ME2A, ME22 (inferredby_MottSimilarity), ME3C, ME32 (inferredby_MottSimilarity), ME3C, ME3C,	3.23 3.19 3.19 3.17 3.17 3.17 3.17 3.17 3.17 3.17 3.17

Table S9 Continued: Cerebellar Bergmann Glia output from RCisTarget for premutation vs. control comparison.

CBL	Estimated Number of Cells	Mean Reads per Cell	Median Genes per Cell	Number of Reads	Valid Barcodes	Sequencing Saturation	Q30 Bases in Barcode	Q30 Bases in RNA Read	Q30 Bases in UMI	Reads Mapped to Genome
1793	4,701	56,278	3,524	264,564,211	95.40%	60.10%	91.80%	93.00%	76.50%	95.70%
5497	5,566	70,949	3,126	394,904,625	97.50%	80.60%	91.70%	87.30%	91.50%	95.10%
5541	5,360	90,127	3,704	483,082,020	96.40%	78.10%	91.50%	87.50%	91.40%	94.40%
5657	5,764	92,365	3,372	532,394,454	97.30%	80.20%	95.40%	92.40%	95.10%	95.90%
AN10723	6,372	46,761	2,571	297,964,738	97.50%	75.90%	95.90%	91.80%	95.40%	93.30%
4806	4,645	90,352	2,154	419,682,889	97.10%	88.30%	90.70%	86.00%	90.80%	93.70%
5319	5,674	71,804	3,746	407,415,252	96.60%	71.30%	91.60%	87.60%	91.50%	94.80%
4555	3,944	70,778	2,652	279,149,167	97.60%	82.00%	95.90%	92.00%	95.50%	92.30%
4664	4,741	47,939	2,737	227,279,509	97.40%	71.30%	91.00%	86.30%	90.80%	94.20%
5006	4,670	35,863	3,107	167,481,681	96.60%	55.80%	91.20%	86.50%	91.00%	94.40%
5212	5,070	49,632	3,002	251,631,846	95.80%	61.40%	91.90%	93.50%	76.40%	96.10%
5746	5,166	41,978	2,909	216,860,497	96.00%	60.10%	92.60%	94.00%	77.70%	96.50%
4751	4,821	117,130	3,534	564,684,721	97.20%	85.40%	95.30%	92.40%	95.10%	95.70%
стх	Estimated Number of Cells	Mean Reads per Cell	Median Genes per Cell	Number of Reads	Valid Barcodes	Sequencing Saturation	Q30 Bases in Barcode	Q30 Bases in RNA Read	Q30 Bases in UMI	Reads Mapped to Genome
1793	3,073	74,963	3,159	230,363,514	95.70%	65.50%	98.40%	91.80%	98.40%	95.70%
5408	4,389	59,487	3,028	261,092,263	97.60%	67.40%	95.90%	91.90%	95.50%	94.10%
5497	5,557	72,214	3,029	401,292,261	97.20%	76.50%	90.80%	85.90%	90.80%	94.50%
5541	5,077	81,152	3,992	412,009,797	96.80%	67.20%	91.60%	87.90%	91.50%	94.70%
5657	4,897	103,724	4,178	507,936,830	97.50%	66.70%	95.40%	92.20%	95.10%	95.90%
4806	4,517	88,308	2,796	398,886,965	97.00%	81.90%	90.80%	85.80%	90.80%	94.10%
5319	5,333	87,892	3,525	468,728,034	96.90%	70.30%	91.60%	87.70%	91.50%	94.70%
5746 (BA22)	2,393	109,360	3,954	261,698,719	96.00%	59.80%	91.70%	93.50%	76.30%	94.90%
4555	2,739	112,219	3,500	307,367,917	97.70%	78.60%	95.90%	91.60%	95.50%	91.80%
4664	2,542	80,464	2,641	204,540,615	97.30%	75.60%	91.10%	86.20%	90.90%	93.90%
4751	3,443	177,604	4,142	611,491,905	97.20%	84.90%	95.30%	92.20%	95.10%	95.40%
5006	3,956	44,910	2,846	177,663,948	97.00%	44.90%	91.00%	86.10%	90.80%	93.70%
5500	4 0 0 0	60.000	4 048	295 802 824	95 50%	43.00%	91.90%	93.60%	76.60%	96.20%

 Table S10:
 Metrics raw output from Cell Ranger pipeline for samples.

Supplemental Information File 1. Linear regression was used to assess the effect of premutation condition and age on premutation and control groups using the equation

 $y=\beta_0+\beta_1x_1+\beta_2x_2$

Nuclei Cluster % = $\beta_0 + \beta_1^*$ condition + β_2^* age

<u>Cortex</u>

Excitatory Neurons							
Parameter				95% CI			P value
estimates	Variable	Estimate	Standard error	(asymptotic)	ltl	P value	summary
ß0	Intercept	-0.9146	6.818	-17.04 to 15.21	0.1341	0.8971	ns
61	Group[PM]	-1.886	6.698	-17.72 to 13.95	0.2815	0.7864	ns
β2	Age	0.2333	0.1024	-0.008771 to 0.4754	2.279	0.0567	ns
Inhibitory Neurons							
Parameter				95% CI			P value
estimates	Variable	Estimate	Standard error	(asymptotic)	t	P value	summary
β0	Intercept	7.891	3.971	-1.500 to 17.28	1.987	0.0873	ns
β1	Group[PM]	-6.573	3.901	-15.80 to 2.652	1.685	0.1359	ns
β2	Age	0.1398	0.05963	-0.001238 to 0.2808	2.344	0.0516	ns
Astrocyte I							
Parameter				95% CI			P value
estimates	Variable	Estimate	Standard error	(asymptotic)	ltl	P value	summarv
ßO	Intercept	18.84	2.779	12.26 to 25.41	6.778	0.0003	***
ß1	Group[PM]	-9.903	2.730	-16.36 to -3.447	3.627	0.0084	**
β2	Age	-0.05304	0.04173	-0.1517 to 0.04563	1.271	0.2443	ns
Astrocyte II							
Parameter				95% CI			P value
estimates	Variable	Estimate	Standard error	(asymptotic)	t	P value	summary

β0	Intercept	7.704	1.198	4.871 to 10.54	6.431	0.0004	***
β1	Group[PM]	-3.501	1.177	-6.284 to -0.7179	2.975	0.0207	*
β2	Age	-0.02099	0.01799	0.02155	1.167	0.2815	ns
Mature Oligoden	drocytes						
Parameter				95% CI			P value
estimates	Variable	Estimate	Standard error	(asymptotic)	t	P value	summary
β0	Intercept	5.296	11.57	-22.06 to 32.66	0.4577	0.6610	ns
β1	Group[PM]	20.44	11.37	-6.435 to 47.32	1.799	0.1151	ns
β2	Age	0.2323	0.1737	-0.1785 to 0.6431	1.337	0.2231	ns
OPC							
Parameter				95% CI			P value
estimates	Variable	Estimate	Standard error	(asymptotic)	t	P value	summary
β0	Intercept	21.66	2.683	15.32 to 28.01	8.074	<0.0001	****
β1	Group[PM]	4.463	2.636	-1.770 to 10.70	1.693	0.1343	ns
β2	Age	-0.2454	0.04029	-0.3407 to -0.1501	6.091	0.0005	***
N.C. 11							
Microglia							
Parameter	Variable	C atimata	Ctondord orrow	95% Cl	141	Dyalua	P value
esumates	Variable				ابا 104 ه		summary
β0		21.57	3.523	13.24 to 29.90	0.124	0.0005	
p1	Group[Pivi]	-0.6021	3.401		0.1740	0.8008	ns
00	Ago	0 1671	0.05290	-0.2921 to -	2 1 5 0	0.0160	*
ρΖ	Age	-0.1671	0.05269	0.04196	3.130	0.0100	
Endothelial							
Parameter							P value
estimates	Variable	Estimate	Standard error	95% CI (asymptotic)) [1	P value	summary
β0	Intercept	0.7394	0.2675	0.1070 to 1.372	2.76	5 0.0279	*
β1	Group[PM]	-0.3206	0.2628	-0.9419 to 0.3007	1.220	0.2619	ns

β2	Age -	0.003812	0.004016-	0.01331 to 0.005685	0.9491	0.3742	ns
Inhibitory Neuron I	Density (Inhibit	ory/Total N	euron percentage)				
Parameter							P value
estimates	Variable E	stimate	Standard error	95% CI (asymptotic)	t	P value	summary
β0	Intercept	0.7645	0.05505	0.6343 to 0.8947	13.89	<0.0001	****
β1	Group[PM] -(0.05218	0.05408	-0.1801 to 0.07569 -0.004535 to -	0.9650	0.3667	ns
β2	Age-0.	002581	0.0008265	0.0006263	3.122	0.0168	*
<u>Cerebellum</u>							
Purkinje							
Parameter							P value
estimates	Variable	Estimate	Standard error	95% CI (asymptotic)	t	P value	summary
β0	Intercept	0.1047	0.1228	-0.1785 to 0.3880	0.8525	5 0.4187	ns
	Condition[PM						
β1]	-0.1568	0.08565	-0.3543 to 0.04070	1.831	0.1045	ns
β2	Age	0.001808	0.001735	0.005810	1.042	0.3279	ns
Bergmann Glia							
Parameter				95% CI			P value
estimates	Variable	e Estimate	Standard erro	r (asymptotic)	t	P value	summary
β0	Intercep Condition[PM	t 4.594 1	1.552	2 1.014 to 8.174	2.959	0.0182	*
β1	-] 2.378	1.082	2 -0.1182 to 4.874	2.197	0.0593	ns
β2	Age	e -0.03712	0.02193	3 0.01346	1.692	0.1290	ns

Granule

Parameter estimates β0 β1 β2	Variable Intercept Condition[PM] Age	Estimate 87.25 -6.366 0.05032	Standard erro 4.91 3.42 0.0693	95% CI or (asymptotic) 2 75.92 to 98.57 5 -14.26 to 1.531 9-0.1097 to 0.2103	t 17.76 1.859 0.7252	P value <0.0001 0.1001 0.4890	P value summary **** ns ns
OPC Parameter							P value
estimates β0	Variable I Intercept Condition[P	Estimate 1.564	Standard error 0.5186	95% CI (asymptotic) 0.3680 to 2.760	t 3.016	P value 0.0167	summary *
β1	M]	0.6912	0.3616	-0.1427 to 1.525 -0.03319 to	1.911	0.0923	ns
β2	Age -	0.01629	0.007327	0.0006017	2.224	0.0568	ns
Astrocyte Parameter estimates β0	Variable Intercept	Estimate 1.084	Standard erro 0.3860	95% Cl r (asymptotic) 0 0.1943 to 1.974	t 2.809	P value 0.0229	P value summary *
β1		0.01825	0.2691	-0.6023 to 0.6388	0.06780	0.9476	ns
β2	Age	-0.002173	0.005453	3 0.01040	0.3984	0.7008	ns
Oligodendrocyte Parameter				95% CI			P value
estimates β0	Variable Intercept Condition[PM	Estimate 1.382	Standard erro 0.509	r (asymptotic) 8 0.2067 to 2.558	t 2.711	P value 0.0266	summary *
β1	.]	0.5364	0.355	4 -0.2833 to 1.356 -0.01750 to	1.509	0.1697	ns
β2	Age	0.0008881	0.007202	2 0.01572	0.1233	0.9049	ns

Microglia							
Parameter				95% CI			P value
estimates	Variable	Estimate	Standard erro	r (asymptotic)	t	P value	summary
β0	Intercept	1.069	0.451	2 0.02846 to 2.109	2.369	0.0453	*
	Condition[PM						
β1	<u></u>	0.1759	0.314	6 -0.5495 to 0.9014	0.5592	0.5913	ns
	-			-0.01935 to			
β2	Age -	0.004652	0.00637	5 0.01005	0.7298	0.4863	ns
Interneuron I							
Parameter estimates	s Variable	Estimate	Standard error	95% CI (asymptotic)	t	P value P	value summary
β0	Intercept	1.028	1.057	-1.409 to 3.466	0.9728	0.3591	ns
β1	Condition[PM]	1.007	0.7371	-0.6927 to 2.707	1.366	0.2090	ns
β2	Age	0.01240	0.01494	-0.02204 to 0.04684	0.8301	0.4306	ns
Interneuron II							
Parameter estimates	s Variable	Estimate	Standard error	95% CI (asymptotic)	t	P value P	value summary
β0	Intercept	1.708	1.187	-1.030 to 4.446	1.439	0.1882	ns
β1	Condition[PM]	1.837	0.8279	-0.07257 to 3.746	2.218	0.0573	ns
β2	Age	-0.005094	0.01677	-0.04378 to 0.03359	0.3037	0.7691	ns

Supplemental Information File 2

Cerebellar top 20 terms for enriched biological processes (BP) and Kyoto Encyclopedia of Genes and Genomes (KEGG) terms for each cellular population with each condition comparison, potential terms of particular interest highlighted with red box.



Astrocyte

Top 20

GO_BP

GO Biological Processes for cerebellar astrocytes demonstrate enrichment of terms implicated in mRNA catabolism (PM vs CON), and protein folding (FXS comparisons).

	Coronavirus disease - COVID-19 -	•	•		
Astrocyte	Oxytocin signaling pathway	•	•		
	MAPK signaling pathway -	•	•	•	
	Estrogen signaling pathway -	•	•	•	
	Amphetamine addiction -	•	•	•	
	Arrhythmogenic right ventricular cardiomyopathy -	•			
	Ribosome -	•	•		
	Lipid and atherosclerosis -		•	•	p.adiust
KEGG	Dopaminergic synapse -		•	•	,,
KLUU	Glutamatergic synapse -		•	•	0.01
	Wnt signaling pathway-		•	•	0.03
	Circadian entrainment -		•	•	0.04
	GABAergic synapse -		•	•	
Top 20	Glucagon signaling pathway-		•	•	GeneRatio
100 20	Long-term potentiation -		•	•	• 0.050
	Protein processing in endoplasmic reticulum -		•	•	0.075
	Propanoate metabolism -		•		0.100
	Rap1 signaling pathway-		•	•	
	Morphine addiction -		•	•	
	Toxoplasmosis -		•	•	
	Legionellosis -		•	•	
	Longevity regulating pathway - multiple species -			•	
	Calcium signaling pathway-			•	
	Parathyroid hormone synthesis, secretion and action -			•	
	Aldosterone synthesis and secretion -			•	
KEGG for cerebellar astrocytes demonstrate enrichme	nt of terms implicated in	66_FXPMvsCON ⁻ (87)	3G_FXPMvsFXS ⁻ (532)	EGG_FXSvsCON ⁷ (343)	
MAPK signaling (PM & FXS comparisons), and neurotr	ansmission (FXS	KEG	KEC	KE	

KEGG for ce MAPK signaling comparisons).



hypoxia and vascular terms (PM comparisons), and protein folding (FXS comparisons).



Adipocytokine signaling pathway-Protein processing in endoplasmic reticulum -Longevity regulating pathway - multiple species -Arrhythmogenic right ventricular cardiomyopathy-Growth hormone synthesis, secretion and action -Thyroid hormone signaling pathway-Phospholipase D signaling pathway

Bergmann Glia

KEGG

Top 20

KEGG for cerebellar Bergmann glia demonstrate enrichment of Wnt signaling, PI3K-Akt signaling, and MAPK signaling (FXS comparisons).

Endothelial	asymmetric stem cell division -	•		
Endothendi	negative regulation of pathway-restricted SMAD protein phosphorylation -	•		
	SMAD protein complex assembly -	•		
	asymmetric cell division -	•		
	positive regulation of chondrocyte differentiation -	•		
	embryonic hindlimb morphogenesis -	•		
	negative regulation of epithelial to mesenchymal transition -	•		
GO BP	positive regulation of cartilage development -	•		p.adjust
_	hindlimb morphogenesis -	•		
	forelimb morphogenesis -	•		0.04751843
	stem cell division -	•		
Top 20	protein peptidyl-prolyl isomerization -	•		GenePatio
	positive regulation of alpha-beta T cell differentiation -	•		 0.33333333
	regulation of chondrocyte differentiation -	•		
	peptidyl-proline modification -	•		
	chaperone-mediated protein folding-	•		
	embryonic digit morphogenesis -	•		
	embryonic pattern specification -	•		
	positive regulation of alpha-beta T cell activation -	•		
	regulation of pathway-restricted SMAD protein phosphorylation -	•		
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GO Biological Processes for endothelial cells demonstrate enrichment of development/morphogenesis and protein folding (PM comparisons).




Morphin	e addiction -	•		
GABAerg	ic synapse -	•		
Estrogen signalir	ig pathway-	• •		
Longevity regulating pathway - multi	ole species -	•	•	
Glutamaterg	ic synapse -	• •	•	
MAPK signalir	ig pathway-	•		
ErbB signalir	ig pathway-	•		
Phosphatidylinositol signal	ing system-	•		
Circadian e	ntrainment -	•	•	p.adiust
Cholinerg	ic synapse -	•	•	
	Ribosome -	•		0.01
Lipid and athe	rosclerosis -	• •		
Calcium signalir	ig pathway-	•		0.02
Axo	n guidance -	• (•	0.03
GnRi	- secretion -	•		GeneRatio
Bacterial invasion of epi	helial cells -	•		• 0.03
Ubiquitin mediated	proteolysis -	•		0.04
Serotonerg	ic synapse -	•	•	0.05
Coronavirus disease -	COVID-19-	•		0.06
Long-term p	otentiation -	•		0.07
Protein processing in endoplasmi	c reticulum -			0.08
Tig	ht junction -		•	
Le	gionellosis -		•	
Oxytocin signalir	ig pathway-		•	
Antigen processing and p	esentation -		•	
Retrograde endocannabinoi	d signaling -		•	
Dopaminerg	ic synapse -		•	
Adrenergic signaling in cardi	omyocytes-	-	•	
Endocrine and other factor-regulated calcium re	absorption -		•	
		_ xs [96]	36)	
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		ž d	XSV	
		μ,		
le celle demonstrate envietnment of evanstic size-line		o' O	EGC	
ie cells demonstrate enrichment of synaptic signaling		Ä	$\overline{\mathbf{X}}$	

KEGG for cerebellar granule cells demonstrate enrichment of synaptic signaling (PM and FXS comparisons).

Granule

KEGG

Interneuron Stell-dependent distratistication protein protein control control protein control protein control protein control protein control control protein control control protein control protein control co		astronalational protain targeting to membrane		•		_
Interneuron dot eventualization protein indigets of intervention in the section of the sect	1 · · ·	Collansiational protein targeting to membrane				
GO_BP Image: Control of the control	Interneuron	protein targeting to EP				
GO_BP readeal removement of the local lation to endoglasmic releaded in the local lation to endoglasmic reledular regions to heredular regions to relead	muunuu	establishment of protein localization to endoplasmic raticulum				
GO_BP Top 200 Collection and protein indication of membrane wat invacient in ansatchied in Registra in Collection and protein indication of membrane wat invacient in ansatchied in Registra in RNA catabolis process purine riforuccies de monophogstate metadolis process purine riforuccies de monophogstate metadolis process in RNA catabolis process in Collection and protein indication of membrane purine riforuccies de monophogstate metadolis process purine riforuccies de monophogstate metadolis process in regulation of celluiar response to heta in equation of celluiar response to heta in equation of neutrane in equation of n		nuclear transcribed mPNA catabolic process, ponsense, mediated decay				
Construction of indication of		nuclear-transcribed mixing catabolic process, nonsense-mediated decay				
GO_BP		protein localization to endoplasmic reliculum				
GO_BOP		protein targeting to membrane -				
GO_BP GO		viral transcription -				
GO_BP GO_BP GO_BP Top 20 Comparisons). Comparisons. Comparisons. Comparisons. Comparisons. Comparisons		viral danscription				
GO_BP GO_BP TOP 20 Comparison of the comparison of the comparis		nuclear-transcribed mRNA catabolic process	_			
GO_BP GO_BP GO_BO GO GO GO GO GO GO GO GO GO G		establishment of protein localization to membrane -	_			
GO_BP Improve distability process BNA distability process outdative physicalitation outdative physical		protein targeting	X	_		
GO_BP Image: Contract of the second of t		mRNA catabolic process	X			
GO_BP TOp 20 Colored Processes for cerebellar interneurons demonstrate enrichment of mRNA catabolism and protein folding (PM comparisons) and protein folding (FXS comparisons).		BNA catabolic process	_	_		GeneRatio
Columna in the intervent of the interven		cytoplasmic translation -		-		Cenertaile
Constrained of the second of t		oxidative phosphorylation -				• 0.05
COD Biological Processes for cerebellar interneurons demonstrate enrichment of mRNA catabolism and protein folding results of a protein folding regulation of neurons and protein folding regulation of intrasmentation of the second of the sec		ATP metabolic process				• 0.10
Cop 20 Chaperone-mediated protein folding regulation of chaperone-mediated protein folding regulation of chaperone-mediated protein folding regulation of chaperone-mediated protein folding response to heat regulation of chaperone-modeling response to heat regulation of chaperone-modeling response to heat response to temperature stimulus- regulation of inclusion body assembly- inclusion body assembly- regulation of inclusions body		nurine ribonucleoside triphosphate metabolic process				0.15
Cop Biological Processes for cerebellar interneurons demonstrate enrichment of mrovad rotein folding inclusion body assently i		purine ribonucleoside monophosphate metabolic process				-
Cop 20 calcium ion transmembrane transport regulation of cellular response to heat calcium ion transmembrane transport regulation of cellular response to heat calcium ion transmembrane transport regulation of cellular response to heat chaperone cofactor-dependent protein refolding response to memory assembly inclusion body assembly regulation of inclusion body regulation		panne hoondeleoside monophosphate metabolic process				
GO Biological Processes for cerebellar interneurons demonstrate enrichment of mRNA catabolism and protein targeting (PM comparisons) and protein folding (FXS comparisons).		chanerone-mediated protein folding -			T	p.adjust
Cop 20 calcum on transmembrane transport regulation of in transmembrane transport regulation of inclusion body assembly inclusion body assembly protein reliding response to the transport regulation of inclusion body assembly protein reliding response to topolymerization regulation of inclusion body assembly protein reliding protein reliding response to topolymerization regulation of inclusion body assembly protein reliding protein reliding protein transport along microtubule microtubule body merization regulation of molecular correct protein regulation of molecular correct protein transport microtubule-based protein transport of regulation of molecular correct protein folding (FXS comparisons).		regulation of cellular response to heat				
GO Biological Processes for cerebellar interneurons demonstrate enrichment of mRNA catabolism and protein folding (PM comparisons) and protein folding (FXS comparisons). 	Top 20	calcium ion transmembrane transport-				- 1e-04
'de novo' protein folding		regulation of ion transmembrane transport		i		20.04
Chaperone cofactor-dependent protein relolding the novo' posttranslational protein folding response to temperature stimulus cellular response to heat response to temperature stimulus cellular response to heat response to included protein negative regulation of inclusion body assembly protein redolding regulation of microtubule cytoskeleton organization regulation of microtubule cytoskeleton organization regulation of microtubule cytoskeleton organization regulation of microtubule polymerization telomere maintenance via telomere lengthening protein transport along microtubule microtubule-based protein transport GO Biological Processes for cerebellar interneurons demonstrate enrichment of mRNA catabolism and protein targeting (PM comparisons) and protein folding (FXS comparisons).		'de novo' protein folding -				20-04
Chaperone cofactor-dependent protein refolding 'de nov' posttranslational protein folding 'de nov' posttranslational protein folding cellular response to temperature stimulus cellular response to table de protein negative regulation of inclusion body assembly- protein refolding response to topologically incorrect protein regulation of microtubule cytoskeleton organization regulation of microtubule cytoskeleton organization regulation of microtubule optimerization protein transport along microtubule microtubule-based protein transport microtubule-based protein transport (FXS comparisons). and protein folding (FXS comparisons).		response to heat-			i	3e-04
GO Biological Processes for cerebellar interneurons demonstrate enrichment of mRNA catabolism and protein fargeting (PM comparisons) and protein folding (FXS comparisons).		chaperone cofactor-dependent protein refolding				40.04
GO Biological Processes for cerebellar interneurons demonstrate enrichment of mRNA catabolism and protein targeting (PM comparisons) and protein folding (FXS comparisons).		'de novo' posttranslational protein folding				40-04
GO Biological Processes for cerebellar interneurons demonstrate enrichment of mRNA catabolism and protein targeting (PM comparisons) and protein folding (FXS comparisons).		response to temperature stimulus			•	
GO Biological Processes for cerebellar interneurons demonstrate enrichment of mRNA catabolism and protein targeting (PM comparisons) and protein folding mRNA catabolism and protein targeting (PM comparisons) and protein folding response). 		cellular response to heat-				
GO Biological Processes for cerebellar interneurons demonstrate enrichment of mRNA catabolism and protein targeting (PM comparisons) and protein folding (FXS comparisons).		response to unfolded protein-			ě	
GO Biological Processes for cerebellar interneurons demonstrate enrichment of mRNA catabolism and protein targeting (PM comparisons) and protein folding (FXS comparisons).		negative regulation of inclusion body assembly				
GO Biological Processes for cerebellar interneurons demonstrate enrichment of mRNA catabolism and protein targeting (PM comparisons) and protein folding (FXS comparisons).		inclusion body assembly			•	
GO Biological Processes for cerebellar interneurons demonstrate enrichment of mRNA catabolism and protein targeting (PM comparisons) and protein folding (FXS comparisons).		protein refolding -			•	
GO Biological Processes for cerebellar interneurons demonstrate enrichment of mRNA catabolism and protein targeting (PM comparisons) and protein folding (FXS comparisons).		response to topologically incorrect protein-				
GO Biological Processes for cerebellar interneurons demonstrate enrichment of mRNA catabolism and protein targeting (PM comparisons) and protein folding (FXS comparisons).		regulation of inclusion body assembly -				
GO Biological Processes for cerebellar interneurons demonstrate enrichment of mRNA catabolism and protein targeting (PM comparisons) and protein folding (FXS comparisons).		regulation of microtubule cytoskeleton organization -			•	
GO Biological Processes for cerebellar interneurons demonstrate enrichment of mRNA catabolism and protein targeting (PM comparisons) and protein folding (FXS comparisons).		regulation of microtubule polymerization or depolymerization -			•	
GO Biological Processes for cerebellar interneurons demonstrate enrichment of mRNA catabolism and protein targeting (PM comparisons) and protein folding (FXS comparisons).		telomere maintenance via telomere lengthening -			•	
GO Biological Processes for cerebellar interneurons demonstrate enrichment of mRNA catabolism and protein targeting (PM comparisons) and protein folding (FXS comparisons).		protein transport along microtubule -				
GO Biological Processes for cerebellar interneurons demonstrate enrichment of mRNA catabolism and protein targeting (PM comparisons) and protein folding (FXS comparisons).		microtubule-based protein transport-				
GO Biological Processes for cerebellar interneurons demonstrate enrichment of mRNA catabolism and protein targeting (PM comparisons) and protein folding day of the targeting (PM comparisons) and protein folding of the targeting of the targeting (PM comparisons) and protein folding of the targeting of t			70	0.0	7.0	
GO Biological Processes for cerebellar interneurons demonstrate enrichment of mRNA catabolism and protein targeting (PM comparisons) and protein folding day			j Dg	374 374	õ S	
GO Biological Processes for cerebellar interneurons demonstrate enrichment of mRNA catabolism and protein targeting (PM comparisons) and protein folding demonstrate enrichment of (FXS comparisons).				(S)	/sC (1	
GO Biological Processes for cerebellar interneurons demonstrate enrichment of mRNA catabolism and protein targeting (PM comparisons) and protein folding defined and defined d			ź	Š	Ś	
mRNA catabolism and protein targeting (PM comparisons) and protein folding	GO Biological Processes for cerebellar	interneurons demonstrate enrichment of	дX	ž.	Ě,	
(FXS comparisons).	mDNA actabalians and protain tarrenting	(DM comparisons) and protoin folding	ш	Ľ,	٩	
(FXS comparisons).	mikina catabolism and protein targeting	(Pivi comparisons) and protein tolding	д .	8	۵	
	(FXS comparisons).		1	0	00	
	().		00	Ū	0	

Ribosome -	•	•		
Coronavirus disease - COVID-19-	•	•		_
Parkinson disease -	•			
Oxidative phosphorylation -	•			
Huntington disease -	•			
Prion disease -	•	•		
Pathways of neurodegeneration - multiple diseases -	•	•		
Amyotrophic lateral sclerosis -	•			
Alzheimer disease -	•			
Diabetic cardiomyopathy-	•			
Non-alcoholic fatty liver disease -	•			
Thermogenesis -	•			
Chemical carcinogenesis - reactive oxygen species -	•			p.adjust
Vibrio cholerae infection -	•			0.01
Retrograde endocannabinoid signaling -	•			0.01
Epithelial cell signaling in Helicobacter pylori infection -	•			0.02
Cardiac muscle contraction -	•			0.03
Collecting duct acid secretion -	•			0.04
Synaptic vesicle cycle -	•			
HIF-1 signaling pathway-	•			GeneRatio
Glutamatergic synapse -		•		• 0.1
Dopaminergic synapse -		•		0.2
Amphetamine addiction -		•		
Circadian entrainment -		•		
Lipid and atherosclerosis -		•	•	
Protein processing in endoplasmic reticulum -		•	•	
Axon guidance -		•		
Long-term potentiation -	1	•		
Calcium signaling pathway-		•		
Nicotine addiction -		•		
Antigen processing and presentation -	4	•	•	
GABAergic synapse -		•		
Estrogen signaling pathway]	•	•	
Legionellosis -		•	•	
	7 @	S (c)	ΖΩ	
	226	195 195	30	
))))	SVSI	
ment of neurodegenerative	AA A	цХ	SX=	
e and axon function (FXS	Ĕ,	Ω 	5	
	ອ່	99	ЮШ	
	KEC	Ш Ш	X	
	<u> </u>			

KEGG for cerebellar interneurons demonstrate enrichment of neurodegenerative terms and prion disease (PM comparisons) and synapse and axon function (FXS comparisons).

VECC

Interneuron

KEGG

	protein targeting to EP				
Later a surren II	protein largeting to ER				
Interneuron II	establishment of protein localization to endonlasmic reticulum				
	protein localization to endoplasmic reticulum				
	SRP-dependent cotranslational protein targeting to membrane				
	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	i	i		
	protein targeting to membrane	`	i		
	establishment of protein localization to membrane-	`	i		
	translational initiation -		i		
	viral transcription -	ě			
	viral gene expression -	ě			
	protein targeting -	•	•		
	nuclear-transcribed mRNA catabolic process -				
	mRNA catabolic process -	•	•		GeneRatio
	RNA catabolic process -	•	•		• 0.05
	cytoplasmic translation -	•	•		0.10
	ribosomal large subunit biogenesis -	•			0.15
	ribosome biogenesis -	•			0.20
	ribosome assembly-	•			0.20
	ribosomal large subunit assembly-	•			
	chaperone-mediated protein folding -		•	•	p.adjust
T 20	protein folding-		•	•	
	'de novo' protein folding		•	•	0.00025
	chaperone cofactor-dependent protein refolding-		•	•	0.00050
	regulation of cellular response to heat-				
	response to temperature stimulus -			-	0.00075
	negative regulation of inclusion body assembly-			1	0.00100
	cellular response to neat-				
	inclusion body assembly -				
	regulation of inclusion body assembly				
	response to unfolded protein-				
	chaperone-mediated protein complex assembly-				
	'de novo' nosttranslational protein folding -				
	response to topologically incorrect protein -				
	protein refolding				
	axo-dendritic transport			•	
	protein transport along microtubule -				
	microtubule-based protein transport -			•	
	transport along microtubule -			•	
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	internet in demonstrate and the first	ž.	≥	XS	
GO BIOIOGICAI Processes for cerebellar	interneuron II demonstrate enrichment of	×.	Ϋ́.	Ш. _ I	
mRNA catabolism and protein targeting	(PM comparisons) and protein folding		<u>م</u> ا	ВР	
(EVS comparisons)		Ξ	e_	o ¹	
(FAS comparisons).		<u>o</u>	00	Ū	
		0	-		





GO Biological Processes for cerebellar microglia demonstrate enrichment of neurotransmitter metabolism (PM comparisons) and protein catabolism (FXS comparisons).

Microglia

GO_BP







	antigen processing and presentation of endogenous peptide antigen	•			
ODC	antigen processing and presentation of endogenous peptide antigen via MHC class I	•			
UPL	antigen processing and presentation via MHC class Ib	•			
	antigen processing and presentation of endogenous antigen	•			
	positive regulation of T cell mediated cytotoxicity	•			
	regulation of T cell mediated cytotoxicity	•			
	regulation of adaptive infinitive response based on somatic recombination of infinitive receptors built non-	•			
	positive regulation of T cell the diated immunity	•			
	T cell mediated cytotoxicity				
	regulation of lymphocyte mediated immunity				
	regulation of adaptive immune response				
	positive regulation of leukocyte mediated cytotoxicity				
	lymphocyte mediated immunity				
	positive regulation of cell killing				GeneRatio
	regulation of 1 cell mediated immunity				0.05
	regulation of leukocyte mediated immunity				0.05
	antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent				• 0.10
	regulation of leukocyte mediated cytotoxicity				0.15
	antigen processing and presentation of exogenous peptide antigen via MHC class I				0.20
	interieron-gamma-mediated signaling patriway-			-	
	changering mediated protein folding				n ediuet
	chaperone-mediated protein rolating		I		p.adjust
	regulation of cellular response to heat		1		
Top 20	inclusion body assembly		I		0.002
	negative regulation of inclusion body assembly		I		0.004
	regative registred to the more than the second				0.000
	resonse to unfolded protein -				0.006
	response to heat-			i	0.008
	cellular response to heat		•	i	
	'de novo' protein folding			• • • • • • • • • • • • • • • • • • •	
	chaperone cofactor-dependent protein refolding		•	•	
	regulation of inclusion body assembly		•	•	
	response to topologically incorrect protein		•	•	
	'de novo' posttranslational protein folding		•	• • • • • • • • • • • • • • • • • • •	
	regulation of protein stability		•		
	protein stabilization		•		
	microtubule polymerization or depolymerization		•	•	
	chaperone-mediated protein complex assembly		•	•	
	regulation of microtubule polymerization or depolymerization		•	•	
	axo-dendritic transport			•	
	regulation of microtubule-based process				
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GU Biological Proces	ses for cerebellar oligodendrocyte progenitors demonstrate		<u>م</u> '	8	
onrichment of antigor	n processing terms (PM comparisons) and protein folding	<u> </u>		o	
	Processing terms (FM compansons) and protein folding	o'	ß	õ	
terms (FXS comparis	ons).	0	0		
•	•				

	Antigen processing and presentation -	•	•	•	
OPC	Thyroid hormone signaling pathway	ĕ	•		_
	Natural killer cell mediated cytotoxicity				_
	Epstein-Barr virus infection -	- Ó			
	Human immunodeficiency virus 1 infection	•			
	Human T-cell leukemia virus 1 infection	•			
	Allograft rejection -	•			
	Graft-versus-host disease -	•			_
	Type I diabetes mellitus-	•			_
	Cell adhesion molecules	•			_
	Autoimmune thyroid disease	•			GeneF
KEGG	Kaposi sarcoma-associated herpesvirus infection-	•			• 0.1
	Mineral absorption -	•			• 0.:
	Viral myocarditis -	•			• 0.:
	Viral carcinogenesis	•			0.:
	Estrogen signaling pathway-		•	•	0.:
	Protein processing in endoplasmic reticulum		•	•	
Tau 20	Aldosterone synthesis and secretion -		•		p.adju:
	Lipid and atherosclerosis		•	•	
· • • • • •	Gastric acid secretion -		•		0.1
	Fluid shear stress and atherosclerosis		•		0.1
	Longevity regulating pathway - multiple species -		•	•	0.1
	Growth hormone synthesis, secretion and action-		•		0.1
	GnRH signaling pathway		•		
	Inflammatory mediator regulation of TRP channels		•		_
	cAMP signaling pathway		•		_
	MAPK signaling pathway		•		_
	Endocrine and other factor-regulated calcium reabsorption		•		_
	Legionellosis		•		
	ErbB signaling pathway		•		
	Aldosterone-regulated sodium reabsorption-				
	Insulin secretion		•		
	Salmonella infection		•		
		_ NC	⁺¹¹⁾ XS ⁻	35) ⁻	
		¹	/sF) (17	SCC SCC	
KEGG for cerebellar oligodendrocyte progenitors demon	strate enrichment of	₩v W	ž	XSV	
antigen processing terms (DM comparisons) and MADI		ЧХ Н	Ĭ.	Ê	
antigen processing terms (PW comparisons) and MAPK s	signaling (FXS	5	ŋ	5	
comparisons).		Ō	Ü	Ē	
		$\overline{\mathbf{X}}$	×		



Supplemental Information File 3

Cortical top 20 terms for enriched biological processes (BP) and Kyoto Encyclopedia of Genes and Genomes (KEGG) terms for each cellular population with each condition comparison, potential terms of particular interest highlighted with red box.

	synapse organization		-		
Actro	axonogenesis				
ASLIUI	axon guidance				
	neuron projection guidance				
	cell-substrate junction assembly		•		
	postsynapse organization				
	positive regulation of peptidyl-tyrosine phosphorylation				
	regulation of small G Pase mediated signal transduction-			-	
	cell-mainx aunesion -				
	regulation of synapse structure of activity				
	cell-substrate adhesion-				
	regulation of cell morphogenesis				
	regulation of neuron projection development				
	negulation of fleuron projection development		—		
	nephron morphogenesis				GeneRatic
GU DP	nositive regulation of neurogenesis				0.025
<u> </u>	positive regulation of cell development				0.023
	negative regulation of pervous system development				• 0.050
	chaperone-mediated protein folding				0.075
	regulation of cellular response to heat				
	regulation of cellular response to heat				
	chaperone cofactor-dependent protein refolding				p.adjust
	'de novo' protein folding				
	regulation of DNA biosynthetic process				0.0004
	response to temperature stimulus				
	'de novo' posttranslational protein folding		T		0.0008
-	cell growth-				0.0012
	establishment of cell polarity		i		
	telomere maintenance via telomerase				0.0016
	RNA-dependent DNA biosynthetic process		•		
	protein refolding -		•	•	
	establishment or maintenance of cell polarity		•		
	regulation of telomere maintenance		•		
	regulation of telomere maintenance via telomerase		•		
	cellular response to heat			•	
	response to heat-			•	
	cell junction organization -			•	
	cell junction assembly -			•	
	modulation of chemical synaptic transmission			•	
	regulation of trans-synaptic signaling			•	
	cellular response to peptide			•	
	response to topologically incorrect protein-			•	
	positive regulation of cellular protein localization			•	
	positive regulation of catabolic process			•	
		Z O	2) (S	N N	
		320	X 75	12.0	
GO Biological Process for astrocyta Labour	parichment for synantic function (PM	;; ;;	vs (1;	/s((1:	
of Diviogical Frocess for astrocyte I shows t	Finicianient for Synaptic function (PM	ź	Σ	(S)	
and FXS comparisons) and protein folding (F)	XS comparisons).	д Т	Ч×	Ě.	
and the companion of and proton forming (in		Ê,	щ	۵'	
		<u>d</u> '	С,	ā	
			<u> </u>	o'	
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		0	6		

Actro I	Axon guidance			-	
ASUOT					
	Inositol phosphate metabolism				
	HIE-1 signaling nathway				
	Morphine addiction			T	
	cAMP signaling pathway				
	Kaposi sarcoma-associated herpesvirus infection		•		
	Circadian entrainment	i			
	Phospholipase D signaling pathway	•			
	Proteoglycans in cancer	•	•	•	p.adiust
KFGG	Rap1 signaling pathway	•		•	
	Lipid and atherosclerosis		•	•	0.01
	MAPK signaling pathway		•	•	0.02
	Estrogen signaling pathway		•	•	0.02
	Longevity regulating pathway - multiple species		•	•	0.03
	Legionellosis -		•	•	
Ton 20	Oxytocin signaling pathway-		•	•	GeneRatic
100 20	Aldosterone synthesis and secretion -		•		• 0.02
· · · ·	Ferroptosis -		•	•	0.04
	TNF signaling pathway		•		0.06
	Thyroid hormone signaling pathway		•		0.08
	cGMP-PKG signaling pathway		•		
	Gastric acid secretion		•		
	Neurotrophin signaling pathway		•	•	
	Osteoclast differentiation		•	•	
	Glutamatergic synapse				
	Hippo signaling pathway				
	Dopaminergic synapse				
	Long-term potentiation				
	Amplietamine addiction				
		70	(0)	70	
KEGG for astrocyte I shows enrichment for axon g synaptic neurotransmission (FXS comparisons).	uidance (PM comparisons) and	66_FXPMvsCON (172	36_FXPMvsFXS (597	EGG_FXSvsCON (566	
		KEG	KE	¥	



GO Biological Process for astrocyte II shows enrichment for synaptic function (PM and FXS comparisons) and nervous system development (FXS comparisons).

Astro II

GO_BP

	Calcium signaling pathway	•			
	Circadian entrainment				
	Choline metapolism in cancer -				
	MAPK signaling pathway		-		
	Oxylocin signaling painway				
	Amphotomics addiction		T T	Ī	
	Phosphalidyilliositol signaling system				
	Filospholipase D signaling pathway				
	l ong-term potentiation -				
	Pan1 signaling nathway				
	ECM-recentor interaction				
	Glioma				p.adiust
KEGG	Mornhine addiction				
ILUU	Arrbythmogenic right ventricular cardiomyopathy				0.0025
	HIE-1 signaling nathway-				0.0050
	Dilated cardiomyopathy		T		0.0075
	Osteoclast differentiation				0.0100
	Ec gamma R-mediated phagocytosis				0.0125
	Lipid and atherosclerosis	Ţ	•	•	0.0125
T 00	Dopaminergic synapse -		i	i	GeneRatic
Ion 20	Longevity regulating pathway - multiple species -		_	i	Cenercate
	Axon guidance -		•	•	• 0.02
•	Toxoplasmosis		•		• 0.04
	Insulin resistance		•		0.06
	Legionellosis -		•		0.08
	Sphingolipid signaling pathway		•		
	Small cell lung cancer-		•		
	Thyroid hormone signaling pathway-		•		
	Estrogen signaling pathway		•		
	Wnt signaling pathway		•	•	_
	Adipocytokine signaling pathway		•		_
	Aldosterone synthesis and secretion		•		
	Hippo signaling pathway-			•	
	Longevity regulating pathway			•	
	Apoptosis -			•	
	Neurotrophin signaling pathway-			•	
	TNF signaling pathway			•	
	Adherens junction -			•	
		2) N	1) (S	N (1	
		(23)	SF)	089	
		Avs	ž	SVS	
		A A	Ч	×.	
		Ĩ,	ш _,	<u> </u>	
		ڻ'	U U	ğ	
VECC for actropyte II about any inhumant for M	ADK signaling (DM and EVC	5 U	Ĕ	Ř	
NEGG for astrocyte II snows enrichment for M	Ark signaling (rivi and rx5	\mathbf{x}	x		

comparisons) and apoptosis (FXS comparisons).

	chaperone-mediated protein folding	•	•
Endo	protein folding -	•	•
	'de novo' protein folding -	•	•
	response to unfolded protein -	•	•
	chaperone cofactor-dependent protein refolding -	•	•
	response to topologically incorrect protein -	•	•
	'de novo' posttranslational protein folding -	•	•
	regulation of cellular response to heat	•	•
	response to heat-	•	• n adjust
GO BP	response to temperature stimulus	•	
	cellular response to heat-	•	• 0.003
	inclusion body assembly-	•	0.006
	protein refolding -	•	• 0.009
	negative regulation of inclusion body assembly-	•	- -
Ton 20	regulation of inclusion body assembly-	•	GeneRatic
100 20	chaperone-mediated protein complex assembly-	•	• 0.03
	protein stabilization -	•	0.06
	regulation of protein stability -	•	•
	negative regulation of response to endoplasmic reticulum stress	•	
	positive regulation of cellular catabolic process	•	
	regulation of RNA splicing		•
	regulation of mRNA metabolic process		•
	viral life cycle -		•
	regulation of DNA biosynthetic process		•
	regulation of mRNA splicing, via spliceosome		•
	interleukin-12-mediated signaling pathway-		•
		88) 88)	O1)
		(11)	(61 (61
		XPX	EXS
GO Biological Process for endothelia	I cells shows enrichment for protein foldir	ng a'	ВР
(PM and FXS comparisons).	· · · · · · · · · · · · · · · · · · ·		
		ŏ	0



KEGG for endothelial cells shows enrichment for longevity (PM and FXS comparisons).



Inh-PVALB

GO_BP

Top 20

GO Biological Process for PVALB I shows enrichment for synaptic function (PM comparisons).

Calcium signaling pathway-				
Giutamatergic synapse			-	
Adrenergic signaling in cardiomyocytes				
Salivary secretion -				
Phosphatidylinositol signaling system -				
Circadian entrainment			•	
CAMP signaling pathway				
Phospholipase D signaling pathway				
Growth hormone synthesis, secretion and action				
				p.adjust
Rap1 signaling pathway				
Inflammatory mediator regulation of TRP channels				0.01
Aldosterone synthesis and secretion				0.02
Long-term potentiation		•	•	0.02
Pancreatic secretion -				0.03
Ras signaling pathway				0.000
Retrograde endocannabinoid signaling	-			GeneRatic
Inositol phosphate metabolism -				• 0.050
Shigellosis -	-			• 0.075
Estrogen signaling pathway				• 0.100
Dopaminergic synapse			-	0.125
GRRH secretion				0.150
Oxytocin signaling pathway				
Lipid and atheroscierosis				
GABAergic synapse			T	
Serotonergic synapse				
Amphotomine addiction			I	
Amphetamine addiction			1	
Protein processing in endoplasmic reliculum				
Raposi sarcoma-associated nerpesvirus infection				
Antigon processing and procentation			Ī	
Antigen processing and presentation				
	scon (84)	/sFXS (231)	scon (123)	
	^₩c	Я́Д	XSV	
ction (PM_and FXS	HX L	Χ <u>.</u>	Ω _.	
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	B	Ú.	Ш	
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Inh-PVALB I

KEGG

Top 20

KEGG for PVALB I shows enrichment for synaptic function (PM and FXS comparisons).

	collular notacsium ion transport			
	cellulai polassiulii ion transport			
ΙΝΝ-ΡΥΔΙΚΙΙ				
	polassium on transport			
	regulation of for lansmerindate transport			
	regulation of ion teneron teneron et a regulation			
	positive regulation of for transmembrane transporter activity			
	regulation of its the requirements and the second			
	regulation of ion transmembrane transporter activity			
	positive regulation of transporter activity			
	regulation of transmembrane transporter activity			
	positive regulation of ion transport	•		
	regulation of potassium ion transmembrane transporter activity			
	regulation of transporter activity	•		p.adjust
	positive regulation of potassium ion transmembrane transporter activity	•		
	positive regulation of cation channel activity	•		0.01
	positive regulation of cation transmembrane transport	•		0.02
	positive regulation of ion transmembrane transport	•		- 0.03
	regulation of cation transmembrane transport	•		0.00
	regulation of potassium ion transmembrane transport	•		0.04
	positive regulation of calcium ion transmembrane transporter activity	•		
	synaptic vesicle transport			CanaDati
-	establishment of synaptic vesicle localization			Generali
lon 20	synaptic vesicle localization			• 0.05
	regulation of synaptic plasticity			• 0.10
	vesicle-mediated transport in synapse-			0.15
	Golgi to plasma membrane protein transport		•	0.20
	anterograde axonal transport		•	0.20
	establishment of protein localization to plasma membrane		•	0.25
	axonal transport-		•	
	establishment of vesicle localization		_	
	Golgi to plasma membrane transport		ē	
	vesicle localization		_	
	axo-dendritic transport		—— ě ———	
	positive regulation of cellular protein localization		Č	
	establishment of protein localization to membrane		ě	
	regulation of synaptic vesicle transport		ŏ	
	vesicle-mediated transport to the plasma membrane		ě	
	post-Golgi vesicle-mediated transport		ě	
	regulation of intracellular transport -			
	modulation of chemical synaptic transmission -			
		70		
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GO Biological Process	for PVALB II shows enrichment for membrane transporter	Ê,	<u>_</u>	
Go biological Flocess		<u>م</u> '	ā	
(PM comparisons) and	synaptic vesicle transport (FXS comparisons).		0	
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	Dhoenhalinges D signaling setting				1
	Phospholipase D signaling pathway				
	Salivary secretion				
	Arrhythmogenic right ventricular cardiomyopathy				
]	Annythinogenic right ventricular cardioniyopathy				
l	Growth hormone synthesis secretion and action				
	Taste transduction				
	Gan junction -				
	Morphine addiction -				
	Aldosterone synthesis and secretion				
	Pancreatic secretion -				
	Thyroid hormone synthesis				
	cGMP-PKG signaling pathway-				
	Proximal tubule bicarbonate reclamation				n adjust
	Axon guidance-	ė			pittajust
L	Estrogen signaling pathway-				- 0.01
	Calcium signaling pathway			i	0.00
	Dilated cardiomyopathy-				0.02
	Phosphatidylinositol signaling system-	•			0.03
l	Inflammatory mediator regulation of TRP channels		•		0.04
	Protein processing in endoplasmic reticulum		•	•	
_	Lipid and atherosclerosis			- Č	GeneRatic
	Serotonergic synapse		•		• 0.0E0
	Oxytocin signaling pathway-		•		0.050
	Retrograde endocannabinoid signaling		•	•	0.075
_	Circadian entrainment		•		0.100
	Long-term potentiation		•		-
	Endocrine and other factor-regulated calcium reabsorption		•		-
	GABAergic synapse		•	•	-
	MAPK signaling pathway				
	Dopaminergic synapse			•	
	Cholinergic synapse			•	
	Antigen processing and presentation -			•	-
	Longevity regulating pathway - multiple species -			•	-
	Type II diabetes mellitus			•	-
	Chemical carcinogenesis - receptor activation -			•	
	Epithelial cell signaling in Helicobacter pylori infection -			•	
	Synaptic vesicle cycle-			•	
	Legionellosis -			•	
		N (O	.s) (0	2 N	
		S &	sF) (25	(14	
		Avs	ž	SVS	
mont for over and	dance (DM comparisons) and MARK	d	ЦX	Х.	
nent for axon gui	uance (FW comparisons) and MAPK	Ĩ,	Ê	<u> </u>	
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KEGG for SST shows enrichn signaling (FXS comparisons).

KEGG

Inh-SST

	SRP-dependent cotranslational protein targeting to membrane				
	cotranslational protein targeting to membrane	`			
	protein targeting to ER	ĕ			
	establishment of protein localization to endoplasmic reticulum	•			
	establishment of protein localization to membrane	•			
	protein targeting to membrane -	•			
	protein localization to endoplasmic reticulum-	•			
	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay				
	protein targeting -				
	regulation of receptor-mediated endocytosis-				
	translational initiation -				
	regulation of postsynantic membrane neurotransmitter receptor levels				
	cognition	ě			
	nuclear-transcribed mRNA catabolic process	ĕ			ConoDatic
GU DP	receptor-mediated endocytosis -	•			Generalic
	learning or memory-	•			• 0.05
	mRNA catabolic process -	•			0.10
	glutamate receptor signaling pathway-	•			
	protein folding -		•	•	n adjuat
	chaperone-mediated protein folding		•	•	p.aujust
	regulation of cellular response to heat				
Ta: 20	chaperone coractor-dependent protein refolding				0.01
	response to topologically incorrect protein -				0.02
	'de novo' nosttranslational protein folding -				0.02
-	response to unfolded protein-				0.03
	response to heat-			ě	
	response to temperature stimulus		•	•	
	cellular response to heat -		•	•	
	protein refolding -		•	•	
	inclusion body assembly-		•	•	
	chaperone-mediated protein complex assembly-		•	•	
	transport along microtubule -				
	microtubule-based transport-			•	
	protein transport along microtubule				
	cytoskeleton-dependent intracellular transport				
	regulation of inclusion body assembly-		Ţ		
	chaperone-mediated autophagy				
	mitochondrial transport			•	
	establishment of protein localization to mitochondrion				
	protein localization to mitochondrion -			•	
		L (2	2) [Z (6	
			21. 21.	0.65	
		vs(s lis	r) Nac(
		Ň.	≥ A	X X	
GO Biological Process fo	r SV/2C Lehows onrichmont for mBNA catabolism (BM	H.	X	۲. E	
GO BIOIOGICAI FIOCESS IO	1 JV20 I SHOWS EIHICHHEIL IUF HIRIVA CALADUISIII (PM	Ľ,		<u>e</u> ,	
comparisons) and proteir	n folding (FXS comparisons).	Ъ.	۳		
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_	memory	•		
	release of sequestered calcium ion into cytosol			
INN-SVZU II	negative regulation of seguestering of calcium ion-	•		
	calcium ion transmembrane transport -	•		
	regulation of seguestering of calcium ion	•		
	sequestering of calcium ion	•		
	calcium ion transmembrane import into cytosol	•		
	learning or memory-	•		
	calcium ion transport into cytosol	•		
	response to isoquinoline alkaloid	•		
	response to morphine	•		
	cytosolic calcium ion transport	•		
	regulation of cation channel activity	•		GeneRatic
	cognition -	•		• 01
GO RD	calcium ion transport -	•		0.1
	positive regulation of cytosolic calcium ion concentration	•		• 0.2
	response to alkaloid	•		0.3
	cellular calcium ion homeostasis -	•		0.4
	maintenance of location -	•		0.5
	retrograde trans-synaptic signaling	•		• • • • • • • • • • • • • • • • • • • •
	regulation of tau-protein kinase activity -		• • • • • • • • • • • • • • • • • • •	
	establishment of protein localization to mitochondrial membrane		Č	p.adjust
Top 20	chaperone-mediated autophagy		Č	0.010
	chaperone-mediated protein complex assembly		`	0.015
•	ionotropic glutamate receptor signaling pathway		Č	0.020
	ERBB2 signaling pathway -		`	0.025
	central nervous system neuron axonogenesis		(0.030
	positive regulation of telomerase activity		_	0.035
	protein refolding		•	
	positive regulation of nitric oxide biosynthetic process		•	
	positive regulation of nitric oxide metabolic process		•	
	regulation of telomerase activity-		•	
	response to cold-		•	
	regulation of nitric-oxide synthase activity		•	
	positive regulation of reactive oxygen species biosynthetic process		•	
	regulation of monooxygenase activity-		•	
	regulation of nitric oxide biosynthetic process			
	positive regulation of DNA biosynthetic process			
	telomere maintenance via telomerase-		•	
	regulation of synaptic transmission, glutamatergic			
		- Ne	2) N	
		(5)	00	
		<u>IX</u>	SNS	
		≥ 0	XS	
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		B	0	
GO Biological Process for	or SV2C II shows enrichment for calcium signaling (PM	o'	Ō	
		0		

GO Biological Process for SV2C II shows enrichment for calcium signaling (PM comparisons) and synaptic transmission (FXS comparisons).



			-		
	establishment of protein localization to membrane		•		
	cotranslational protein targeting to membrane		•		
	protein targeting to ER		•		
	establishment of protein localization to endoplasmic reticulum	•	•		
	protein localization to endoplasmic reticulum -	•			
	localization within membrane -	•			
	protein targeting to membrane -	•	•		
	SRP-dependent cotranslational protein targeting to membrane -	•	•		
	glutamate secretion -	•			
	regulation of amine transport -	•			
	neurotransmitter transport -	•			
	amine transport -	•			
	neurotransmitter receptor transport, endosome to postsynaptic membrane -	•			
	neurotransmitter receptor transport, endosome to plasma membrane	•			GeneRatic
	protein targeting -	•	•		• 0.025
	modulation of chemical synaptic transmission	•			0.050
	regulation of trans-synaptic signaling	•			0.050
	acidic amino acid transport -	•			0.075
	endosome to plasma membrane protein transport -	•			0.100
	protein transport within lipid bilayer	•			0.125
	protein folding -		•		
	regulation of cellular response to heat		•	— — — — — — — — — — — — — — — — — — —	
	chaperone-mediated protein folding		•	• • •	p.adjust
<u>, 70</u>	response to temperature stimulus		•		
JZU	response to topologically incorrect protein		•	— — — — — — — — — — — — — — — — — — —	0.001
	chaperone cofactor-dependent protein refolding -			•	
	'de novo' protein folding		•	•	- 0.002
	'de novo' posttranslational protein folding		•		0.003
	response to unfolded protein-		•		
	response to heat		•		
	mRNA catabolic process		•	T	
	cellular response to heat		•		
	translational initiation		•		
	protein refolding -			_	
	chaperone-mediated autophagy				
	cytoskeleton-dependent intracellular transport			_	
	transport along microtubule			i	
	microtubule-based transport			i	
	chaperone-mediated protein complex assembly				
	negative regulation of inclusion body assembly				
	axo-dendritic transport				
	inclusion body assembly			i	
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GO Biological Process for VIP	snows enrichment for synaptic transmission (PM	<u>م</u>	El	0'	
comparisons) and protein fold	ling (FXS comparisons)	<u>O</u>	0	G	
companisons, and protein 1010		0	-		

Inh-VIP

GO_BP

	Synaptic vesicle cycle -	•	•	•	
INN-VIP	Ribosome -	•	•		
	Coronavirus disease - COVID-19-	•	•		
	Epithelial cell signaling in Helicobacter pylori infection-	•			
	Lipid and atherosclerosis -		•	•	
	Protein processing in endoplasmic reticulum-		•	•	
	Parkinson disease -		•		
	Gastric acid secretion -		•	•	
	Estrogen signaling pathway-		•	•	GeneRatic
KEGG	Pathways of neurodegeneration - multiple diseases -		•		• 0.04
NLUU	Oocyte meiosis-		•	•	• 0.06
	Insulin secretion -		•		0.08
	Oxytocin signaling pathway-		•	•	0.10
	Salivary secretion -		•		•
T 00	Prion disease -		•		p.adjust
100 20	Circadian entrainment-		•	•	0.01
	Alzheimer disease -		•		0.02
	Cholinergic synapse-		•		0.03
	Dopaminergic synapse-		•		0.04
	Salmonella infection -				
	Inflammatory mediator regulation of TRP channels				
	l egionellosis -				
	Antigen processing and presentation -				
	Longevity regulating nathway - multiple species -			I	
	Ampletamine addiction			I	
				I	
	Nourotrophin signaling pathway			I	
	Neurou opinin signaling paulway	70			
		(53)	3FXS 265	CON (133	
		WNS	svM's	SVS (
		IdX	НХР	Ĕ,	
KEGG for VIP shows enrichment for	synaptic vesicles, prion, and	ڻ ت	Ъ	00	
neurodegenerative terms (PM and F)	KS comparisons).	KEG	KEC	Ϋ́Ε	



	Coronavirus disease - COVID-19-	•	•		-
Microglia	Ribosome -	•	•	_	
iviici oglia	Inflammatory bowel disease -	•			
	Leishmaniasis -	•			
	Th17 cell differentiation -	•			
	Legionellosis -	•	•	-	
	Toll-like receptor signaling pathway-	•	•		
	Measles -	•	•		
	HIF-1 signaling pathway	•	•		
	JAK-STAT signaling pathway	•			
	Toxoplasmosis -	•			GeneRatic
KF(1(1	Acute myeloid leukemia	•			• 0.025
	PD-L1 expression and PD-1 checkpoint pathway in cancer	•	•	•	• 0.050
	Lipid and atherosclerosis	•	•	•	0.075
	Phagosome -	•			0.100
	Tuberculosis -	•	•	•	
	Shigellosis -		•		p.adjust
Ton 20	Kaposi sarcoma-associated herpesvirus infection -		•	•	-
	Salmonella infection -		•	•	0.01
•	Yersinia infection -		•	•	0.02
	Platelet activation -		•	•	0.03
	Longevity regulating pathway - multiple species -		•	•	0.04
	Osteoclast differentiation -		•	•	
	NOD-like receptor signaling pathway		•		
	Pathogenic Escherichia coli infection		•	•	
	Fc gamma R-mediated phagocytosis		•	•	
	Human immunodeficiency virus 1 infection		•		
	Phospholipase D signaling pathway			•	
	MAPK signaling pathway			•	
	Estrogen signaling pathway			•	
	Fluid shear stress and atherosclerosis			•	
	B cell receptor signaling pathway				
		- Z (0	- S) (6	Z Ô	
		SCC (27	(59) (59	(90	
		Š	Ň	Svs	
		ЧХ	ΕXF	۵,	
KEGG for microalia shows enrichment for inf	ection response (PM comparisons)	۳ ۵	g	0 9	
and MAPK signaling (FXS comparisons).		KEG	KEG	Ū ¥	

	negative regulation of supramolecular fiber organization	•			
	telencephalon development	•			
	cotranslational protein targeting to membrane -		•		
	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay		•		
	SRP-dependent cotranslational protein targeting to membrane -		•		
	establishment of protein localization to endoplasmic reticulum -		•		
	protein targeting to ER -		•		
	protein localization to endoplasmic reticulum-				
	translational initiation -				
	protein targeting to membrane				
	nuclear-transcribed mRNA catabolic process				
	establishment of protein localization to membrane				p.adjust
DD	mRNA catabolic process				
	viral transcription -				
	RNA catabolic process				0.01
	viral gene expression -				
	protein targeting				0.02
	cytoplasmic translation -				
	protein tolding -				
	chaperone-meulateu protein loiding-				GeneRatic
~ 20	synapse organization				• 0.03
	chaperone cefacter dependent protein refolding		-		0.04
	'de pove' protein folding			I	0.04
	response to heat-				0.05
	'de novo' nosttranslational protein folding -				0.06
	regulation of cellular response to heat				0.07
	response to temperature stimulus				
	response to unfolded protein-				
	regulation of protein stability				
	protein stabilization			i	
	cellular response to heat				
	protein refolding -				
	response to topologically incorrect protein			•	
	axonogenesis			ě	
	divalent metal ion transport-				
	divalent inorganic cation transport				
	calcium ion transmembrane transport -			ě	
		Z	S @	Zô	
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		c)	lvs (;	r)	
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			۵. ^۱	BP	
GO Biological Processes for oligo	dendrocyte shows enrichment for protein folding	商	е -	0	
(FXS comparisons).		0 O	00	Ō	

MOL

Top 20

GO_BP

•	Glutamatergic synapse
• • • • • • • • • • • • • • • • • • •	Arrhythmogenic right ventricular cardiomyopathy-
• •	Axon guidance -
• • • • • • • • • • • • • • • • • • • •	Ribosome -
• • • • • • • • • • • • • • • • • • • •	Coronavirus disease - COVID-19-
• •	Dopaminergic synapse
• •	Amphetamine addiction
• •	Parkinson disease
• p.adjust	Adherens junction -
• • • • • • • • • • • • • • • • • • • •	Long-term potentiation
	Prion disease -
• • 0.03	Circadian entrainment -
• • 0.04	Rap1 signaling pathway-
• • • • • • • • • • • • • • • • • • •	Oxytocin signaling pathway-
GeneRatic	Pathways of neurodegeneration - multiple diseases
• 0.05	Lipid and atherosclerosis -
• 0.07	Alzheimer disease
• 0.09	Gastric acid secretion -
• •	Salmonella infection -
• •	Estrogen signaling pathway-
• • • • • • • • • • • • • • • • • • •	Fluid shear stress and atherosclerosis-
• • • • • • • • • • • • • • • • • • •	Legionellosis -
•	Focal adhesion -
• • • • • • • • • • • • • • • • • • •	Adrenergic signaling in cardiomyocytes
• • • • • • • • • • • • • • • • • • •	GABAergic synapse
•	Platelet activation -
FXPMvsCON [106]	
KEGG_F	t for prion and neurodegenerative

KEGG for oligodendrocyte shows	enrichment for	prion and	neurodegener	ative
terms (FXS comparisons).				

MOL

KEGG

axonogenesis	•			
establishment of protein localization to membrane -		•	•	
protein localization to endoplasmic reticulum -		•		
establishment of protein localization to endoplasmic reticulum		•		
cotranslational protein targeting to membrane -		•		
regulation of metal ion transport -		•		
protein targeting to ER -		•		
SRP-dependent cotranslational protein targeting to membrane -		•		
regulation of ion transmembrane transport -		•		
regulation of neurotransmitter levels		•	•	
clear-transcribed mRNA catabolic process, nonsense-mediated decay		•		p.adiust
neurotransmitter transport		•	•	produjeno e
chaperone-mediated protein folding -		•	•	0.00
vesicle-mediated transport in synapse -		•	•	0.00
modulation of chemical synaptic transmission		•	•	0.00
regulation of trans-synaptic signaling		•	•	0.00
neural nucleus development		•		0.00
translational initiation -		•		Com Da
synaptic vesicle cycle		•	•	Genera
regulation of cation transmembrane transport		•		• 0.05
regulation of transmembrane transporter activity				0.07
protein folding			•	0.10
regulation of cellular response to heat				0.12
regulation of synaptic plasticity				
regulation of neurotransmitter transport				
response to temperature stimulus				
'de novo' protein folding -				
cellular response to heat-				
signal release from synapse				
regulation of synaptic vesicle cycle				
regulation of synaptic vesicle cycle				
Synaplic vesicle exocytosis	70		70	
	(95)	vsFXS (352)	/sCON (217)	
	WWX	XPM	FXS	
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I shows enrichment for protein folding (FXS	Ъ		o	
	0 [']	O U	ŏ	

Neu L4 I

GO_BP

GO Biological Processes for comparisons).
	Phosphatidylinosital signaling system				
	Neurotrophin signaling system	X		•	
	Adrenergic signaling in cardiomyocytes	ă	T	-	
	Inflammatory mediator regulation of TRP channels				
	Glutamatergic synapse				
	inositol phosphate metabolism-				
	Shigellosis	•		•	
	Circadian entrainment -	•			
	AGE-RAGE signaling pathway in diabetic complications	•			
	Cholinergic synapse				
	Sphingolipid signaling pathway				
	Growth hormone synthesis, secretion and action -				
	MICRORIAS IN CANCER-				
					GeneRatic
			-		• 0.03
JU	CAMP signaling nathway -				0.05
	Estrogen signaling pathway		•		0.06
	Beneficial and Beneficial Action		-		0.09
	Protein processing in endoplasmic reticulum -		•	•	0.12
	Ribosome -		ě	-	0.15
	Coronavirus disease - COVID-19		ě – – – – – – – – – – – – – – – – – – –		•
	Lipid and atherosclerosis		•	•	
	Prion disease		•		p.adjust
n 20	Salmonella infection -		•	•	
520	Fluid shear stress and atherosclerosis		•	•	- 0.01
	Amphetamine addiction		•	•	0.02
	GABAergic synapse		•	•	0.03
	Bacterial invasion of epithelial cells		•		0.04
	Synaptic vesicie cycle				0.04
	Pathways of neurodegeneration - multiple diseases			-	
	Citytoin signaling patiway				
	Huntington disease				
	l ongevity regulating natiway - multinle species -		T		
	Vasoressin-regulated water reabsorption		•		
	Oocyte meiosis -			•	
	Mitophagy - animal -			•	
	Gastric acid secretion -			•	
	Vibrio cholerae infection			•	
	Kaposi sarcoma-associated herpesvirus infection			•	
	Salivary secretion -			•	
	Epithelial cell signaling in Helicobacter pylori infection			•	
	Glioma -			•	
			(2) (2)	E SN	
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KECC for Nou I 4 Jahowa	envielment for neurotronomicsion (DM comparisons) and		ບ່	0	
REGG for Neu L4 I Shows (enforment for neurotransmission (PW comparisons) and	<u> </u>	9	Ŭ	
infection (FXS comparison	IS).	Щ. Щ.	X	<u> </u>	
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Neu L4 I

KEGG

	synaptic vesicle priming	•			
	regulation of neurotransmitter levels	_	•		
	negative regulation of peptidyl-threonine phosphorylation			T	
	neuron projection arborization				
	modulation of chemical synaptic transmission			•	
	regulation of trans-synaptic signaling		`	`	
	regulation of ion transmembrane transport		_		
	regulation of cation transmembrane transport		i		
	regulation of transmembrane transporter activity		ě		
	regulation of transporter activity				
	regulation of metal ion transport-				
	regulation of ion transmembrane transporter activity				
	regulation of postsynaptic neurotransmitter receptor activity		T		p.adjust
	regulation of heart contraction				
	regulation of blood circulation				- 0.01
	synaptic vesicle cycle			•	0.01
	regulation of neurological system process				- 0.02
	neurotransmitter secretion				0.0E
	signal release from synapse				
	multicellular organismal signaling				
	vesicle-mediated transport in synapse				GeneRatic
	heart contraction				• 0.025
	heart process				• 0.050
	regulation of synaptic plasticity				0.075
	axonogenesis				0.010
L	establishment of protein localization to membrane				0.100
	synantic vesicle exocytosis				0.125
	positive regulation of phosphoprotein phosphatase activity				
	synantic vesicle transport				
	establishment of synaptic vesicle localization				
	calcium ion regulated exocytosis				
	regulation of synantic vesicle cycle				
	response to pentide hormone				
	nositive regulation of cAMP-mediated signaling				
	cellular response to pentide hormone stimulus				
	cellular response to peptide normone stimulas				
	synantic vesicle localization				
	neurotransmitter transport				
		72)	21) 21)	37) 37)	
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I Alleho	we enrichment for expantic vesicles (DM	ВР	''''''''''''''''''''''''''''''''''''''	E C	
	we entrement for synaptic vesicles (PM	0	o'	00	
		ŏ	Ċ	-	

Neu L4 II

GO_BP

Top 20

GO Biological Processes for Neu L4 II shows enrichment for synaptic vesicles (PM and FXS comparisons).

Vibrio cholerae infection -	•
Fluid shear stress and atherosclerosis -	•
Epithelial cell signaling in Helicobacter pylori infection -	
Rapi signaling pathway-	
Glioma	•
Gastric acid secretion -	GeneRatic
Synaptic vesicle cycle	• 0.10
Salivary secretion -	• 0.15 • 0.20
Estrogen signaling pathway-	• • • •
Phosphatidylinositol signaling system	p.adjust
Top 20	0.01
	0.02
Pliagusuitie	0.02
Long-term potentiation	• • • • • • • • • • • • • • • • • • • •
Lipid and atherosclerosis -	•
Shigellosis -	•
Insulin secretion -	•
Pathways of neurodegeneration - multiple diseases	
Insulin signaling pathway-	•
Ec gamma R-mediated nhagocytosis -	
	70
	(55)
	SNSX
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	establishment of protein localization to endoplasmic reticulum	•		•	
	protein targeting to ER	•		•	
	protein localization to endoplasmic reticulum	•		•	
	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	•		•	
	protein targeting	•		•	
	cotranslational protein targeting to membrane	•		•	
	protein targeting to membrane	•		•	
	SRP-dependent cotranslational protein targeting to membrane	1			
	establishment of protein localization to membrane			•	
	endomembrane system organization			_	
	huclear-transcribed mRNA catabolic process				
	mRNA catabolic process			•	
	cytoskeleton-dependent intracellular transport				p.adjust
	protein polymerization				
	Goigi vesicie transport				5.0.01
	trongent along migrotuble				5.0e-0
	transport along microtubule				1 0e-0f
	microtubule-based transport	1			1.00 00
					1.5e-0(
	modulation of chamics transmission				
	rodulation of trans synaptic transmission				
	regulation of trains-synaptic signaling				GeneRatic
To: 20	regulation of synaptic plasticity				• 0.025
	calcium ion regulated executoria			-	• 0.025
	vesicle-mediated transport in synapse				• 0.050
	regulation of synaptic vesicle cycle				0.075
	regulation of ion transmembrane transmot				0.100
	learning or memory		X		0.105
	regulation of synapse structure or activity		`		0.125
	regulation of synapse organization		i		
	synantic vesicle localization				
	nostsvnapse organization		`		
	continu		`		
	synaptic vesicle transport		i		
	establishment of synaptic vesicle localization				
	dendrite morphogenesis		i		
	synaptic vesicle exocytosis				
	learning		ě		
	viral transcription-		T	•	
	viral gene expression			•	
	dendrite development			•	
	regulation of neuron projection development			•	
		78	500	7.2	
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GU Biological Processes	s for NKGN shows enrichment for protein targeting (PM and		1	Q'	
FXS comparisons)		0	ğ	U	
		0			

Pathways of neurodegeneration - multiple diseases	•			
Parkinson disease	•			
Ribosome-				
Coronavirus disease - COVID-19-				
Prion disease				
Amyotrophic lateral sclerosis				
Alzheimer disease	ĕ			
Oxidative phosphorylation -	——————————————————————————————————————		-	
Thermogenesis	•			
Ubiquitin mediated proteolysis -	•			
Chemical carcinogenesis - reactive oxygen species -				
Salmonella infection -			-	
Mitophagy - animal				
Autophayy - animati-				GeneRatic
Adherens junction -				• 0.03
Tight junction				• 0.05
Diabetic cardiomyopathy -	i		•	0.06
Spinocerebellar ataxia				0.09
Dopaminergic synapse		•	•	0.12
Long-term potentiation		•	•	0 15
Oxytocin signaling pathway-		-	•	0.10
Amphetamine addiction -				
Insuin secretion -				o.adjust
Adrenergic signaling in cardiomyocytes				
cAMP signaling nathway-				- 0.0005
Circadian entrainment-		X		
Vibrio cholerae infection -				0.0010
Gastric acid secretion -				0.0015
Hippo signaling pathway -		•		0.0015
Renin secretion -		•		
Inflammatory mediator regulation of TRP channels				
Cocaine addiction -				
Giucagon signaling pathway-				
Diatelet activation -				
Ran1 signaling nathway-		_		
Dilated cardiomyopathy -		`		
MAPK signaling pathway-	1	Ť	•	
Retrograde endocannabinoid signaling			•	
ErbB signaling pathway-			•	
Gap junction -			•	
Renal cell carcinoma -				
Morphine addiction				
	NC (94	34) XS	32) 32	
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odegeneration (PM and FYS	ഠ	ບູ່	00	
ouegeneration (Fill and FAG	Ō	U U	Щ	
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Neu NRGN

KEGG

Top 20

KEGG for NRGN shows enrichment for neurodegeneration (PM and FXS comparisons).

	vesicle-mediated transport in synapse-			
Nou NTNG2				
	neuron projection extension -			
	regulation of cellular component size			
	synantic vesicle localization			
	regulation of cell mornhogenesis involved in differentiation			
	regulation of cell molphogenesis involved in differentiation			
	neurotransmitter secretion			
	vesicle localization -			
	signal release from synapse			
	regulation of neurotransmitter levels			GeneF
	regulation of cell size			• 0.:
_				• 0.:
	regulation of cell mornhogenesis			• 0
	synantic vesicle transport			p.adius
	establishment of synaptic vesicle localization			piadja
Top 20	establishment of vesicle localization			0.0
100 20	calcium ion regulated exocytosis			0.0
antigen processing	and presentation of exogenous pentide antigen via MHC class II			0.
anagen processing	easome-mediated ubiquitin-dependent protein catabolic process			
prot	regulation of peurological system process			
	axonogenesis			
	negative regulation of axon extension -			
	developmental cell growth			
	developmental growth involved in morphogenesis			
	axon quidance -			
	neuron projection guidance -			
	positive regulation of neurological system process			
	negative regulation of axonogenesis			
		7.2		
		(2240)	(12 (12	
		NVS (ŠÂW.	
		IdX	d X	
GO Biological Processe	s for NTNG2 shows enrichment for synaptic fun	ction (PM 🔤	E C	
comparisons).		09	ŏ	



	synapse organization-	•		•	•	-
	axonogenesis-			•	•	
ULI	regulation of neuron projection development	7		•		
	modulation of chemical synaptic transmission -					
	regulation of trans-synaptic signaling-				-	
	dendrite development					
	onshoothmont of nourons			I		
	avon ensheathment			I		
	regulation of cell morphogenesis involved in differentiation -					
	regulation of cell morphogenesis involved in differentiation	_		—		
	axon guidance -			-		
	positive regulation of neurogenesis	ě		•		
	neuron projection guidance			Ţ		-
	regulation of membrane potential					GeneRatic
	regulation of GTPase activity-					0.03
	cell junction organization -	•		•		
	negative regulation of nervous system development-	•				0.04
	regulation of axonogenesis	•				0.05
	postsynapse organization-	•				0.06
	regulation of supramolecular fiber organization			•		0.07
	positive regulation of cell projection organization					
	regulation of transporter activity-					
	neuron migration-			1		p.adjust
Top 20	yildi cell uliferentiation -					
	protein localization to cell periphery-					- 2e-07
	regulation of transmembrane transporter activity			1		
	dendrite mornhorenesis -			Ţ		4e-07
	cotranslational protein targeting to membrane				•	
	SRP-dependent cotranslational protein targeting to membrane				i	6e-07
	establishment of protein localization to endoplasmic reticulum				ě	
	protein targeting to ER-				Ó	
nuc	clear-transcribed mRNA catabolic process, nonsense-mediated decay-				•	
	protein localization to endoplasmic reticulum				•	-
	establishment of protein localization to membrane				•	
	translational initiation -				•	
	protein targeting to membrane					
	nuclear-transcribed mRNA catabolic process					
	protein targeting-					
	Viral transcription					
	mRNA catabolic process					
	PNA catabolic process					
	cytoplasmic translation					
]
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GO BIOlOgical Processes for OLI show	vs enrichment for synaptic function and	۳		Ξ_	o'	
myelination (PM comparisons)		<u>O</u>		0	U	
		0		-		

Diabetic cardiomyopathy Oxidative phosphorylation cGMP-PKG signaling pathway				
Diabetic cardiomyopathy- Oxidative phosphorylation				
Diabetic cardiomvonathy -				
			-	
Paulways of neurodegeneration - multiple diseases				
Lipid and atheroscierosis				
Parkinson disease				
Coronavirus disease - COVID-19-				
Ribosome -				
Wnt signaling pathway		•		
Bacterial invasion of epithelial cells		•		• ••
Proteoglycans in cancer				0.10
Rap1 signaling pathway		•		0.08
Amphetamine addiction				0.06
Long-term potentiation				• 0.04
Gastric acid secretion				GeneRatic
MAPK signaling pathway	-			
Cell adhesion molecules	•			6e-04
Retrograde endocannabinoid signaling	•			4e-04
Salivary secretion -	•	•	•	
Dopaminergic synapse -	•	•	•	2e-04
Calcium signaling pathway	•			
Adherens junction	i	i		p.adjust
Oxytocin signaling pathway				
Addesterone synthesis and secretion				
GABAErgic synapse				
CARAcress Superso				
cAMP signaling pathway				
Arrhythmogenic right ventricular cardiomyopathy	•			
Circadian entrainment	•	•		
Phospholipase D signaling pathway	•			
Insulin secretion-	•	•	•	
Morphine addiction -		•		
Axon guidance-		•		
	Glutamatergic synapse Axon guidance Morphine addiction Insulin secretion Phospholipase D signaling pathway Circadian entrainment Arrhythmogenic right ventricular cardiomyopathy cAMP signaling pathway Pancreatic secretion GABAergic synapse Adrenergic signaling in cardiomyocytes Aldosterone synthesis and secretion Oxytocin signaling pathway Adherens junction Calcium signaling pathway Dopaminergic synapse Salivary secretion Retrograde endocannabinoid signaling Cell adhesion molecules MAPK signaling pathway Gastric acid secretion Hippo signaling pathway Long-term potentiation Amphetamine addiction Rap1 signaling pathway Proteoglycans in cancer Bacterial invasion of epithelial cells Wnt signaling pathway Ribosome Coronavirus disease - COVID-19 Parkinson disease Lipid and atherosclerosis Pathways of neurodegeneration - multiple diseases Alzheimer disease	Glutamatergic synapse Axon guidance Morphine addiction Insulin secretion Phospholipase D signaling pathway Circadian entrainment Arrhythmogenic right ventricular cardiomyopathy cAMP signaling pathway Pancreatic secretion GABAergic synapse Adrenergic signaling in cardiomyocytes Aldosterone synthesis and secretion Oxytocin signaling pathway Adherens junction Calcium signaling pathway Dopaminergic synapse Sallvary secretion Retrograde endocannabinoid signaling Cell adhesion molecules MAPK signaling pathway Gastric acid secretion Hippo signaling pathway Corem potentiation Amphetamine addiction Retrograde endocannabinoid signaling Cell adhesion molecules MAPK signaling pathway Corent potentiation Amphetamine addiction Rap1 signaling pathway Ribosome Coronavirus disease - COVID-19 Parkinson disease Lipid and atherosclerosis Pathways of neurodegeneration - multiple diseases Prion disease Prion disease Prion disease	Glutamatergic synapse Axon guidance Morphine addiction Insulin secretion Insulin secretion Phospholipase D signaling pathway Circadian entrainment Insulin secretion Arrhythmogenic right ventricular cardiomyopathy cAMP signaling pathway Insulin secretion GABAergic synapse Insulin secretion Adrenergic signaling in cardiomyocytes Insulin secretion Oxytocin signaling pathway Insulin secretion Calcium signaling pathway Insulin secretion Calcium signaling pathway Insulin secretion Retrograde endocannabinoid signaling Insulin secretion Gastric acid secretion Insulin secretion Retrograde endocannabinoid signaling Insulin secretion Gastric acid secretion Insulin secretion Hippo signaling pathway Insulin secretion Raph signaling pathway Insulin secretion Hippo signaling pathway Insulin secretion Rapi signaling pathway Insulin secretion Ribosome Insulin secretion </td <td>Glutamatergic synapse Axon guidance Image: Secretion - Image:</td>	Glutamatergic synapse Axon guidance Image: Secretion - Image:

KEGG for OLI shows enrichment fo comparisons).

KEGG

OLI

	protoin folding			
	chaperene mediated protein folding			
	chaperone-mediated protein rolding			
•	response to temperature stimulus			
	chaperone cofactor-dependent protein refolding			
	'de novo' protein folding			
	inclusion hody assembly -			
	'de novo' posttranslational protein folding			
	regulation of cellular response to heat-			
	response to heat			
	regulation of inclusion body assembly	T		
	response to unfolded protein-			p.adjust
	regulation of neuron projection development -	`		
GO RD	response to topologically incorrect protein -			0.00005
	ossification -			0.00010
	protein stabilization -	T		0.00015
	extracellular matrix organization -			0.00018
				0.00020
	negative regulation of inclusion body assembly-			
	muscle tissue development -			GeneRatio
To: 20	cell-substrate adhesion -	-		• 0.01
	cell substrate adhesion			• 0.02
	regulation of small GTPase mediated signal transduction			0.03
	cell-matrix adhesion -			0.04
	axon quidance -			0.05
	cell junction assembly-			0.05
	neuron projection quidance -			0.00
	axonogenesis -			
	protein localization to cell periphery -			
	response to pentide hormone -			
	regulation of cell-substrate adhesion -			
	adherens junction organization			
	regulation of actin filament-based process			
	regulation of Ras protein signal transduction			
	homotypic cell-cell adhesion			
	extracellular structure organization			
	muscle organ development			
		577 577	33.0	
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GO for OLIL shows anrichment for n	rotein folding (PM comparisons)	B	0	
		0	Ċ	

	Focal adhesion -		
	PI3K-Akt signaling pathway-		-
	Lipid and atheroscierosis		
	Calcium signaling pathway		
	Circadian entrainment		
	Circadian entrainment		
	Folein processing in endoplasmic reliculum		
	ECM-receptor interaction-		
	Rapi signaling painway		
KEGG	Salivary secretion		GeneRat
	Small cell lung cancer-		• 0.04
	EGFR tyrosine kinase innibitor resistance		• 0.06
	Estrogen signaling pathway		0.08
	Ampnetamine addiction -		
	Prostate cancer		p.adjust
	Purine metabolism -		
lon 20	Adherens junction -		0.01
100 20	Amoeblasis-		0.02
	Proteoglycans III cancer		
	Bacterial invasion of epithelial cells		0.03
	Regulation of actin cytoskeleton-		
	Armythmogenic right ventricular cardiomyopathy-		
	Axon guidance		
			I
	Hypertrophic cardiomyopathy		
	Siligeilosis-		
	Human papilionavirus intection		
	MARK Signaling pathway		
	Phospholipase D signaling pathway		
	Oxytocin signaling pathway-		
		31) 31)	NO:16
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REGG for ULII shows enrichment for axon guida	nce (FXS comparisons).	(EC	Ж
		<u>~</u>	



GO for OPC shows enrichment for cognition (PM comparisons) and myelination (FXS comparisons).

OPC

GO_BP

	Bacterial invasion of epithelial cells	•			
	Cell adhesion molecules -	•			
	Thyroid hormone signaling pathway-	•			
	Glutamatergic synapse -		•	•	
	MAPK signaling pathway-		•	•	
[Dopaminergic synapse -		•	•	
	Oxytocin signaling pathway-		•	•	
	Adrenergic signaling in cardiomyocytes -		•	•	
	Estrogen signaling pathway-		•	•	n ediuet
	GnRH signaling pathway-		•	•	p.adjust
	Long-term potentiation -		•	•	0.01
	Amphetamine addiction -		•	•	0.02
	Insulin secretion -		•	•	0.03
	Circadian entrainment -		•		0.04
	Prostate cancer-		•		
	Salmonella infection -		•	•	GeneRatic
	Parathyroid hormone synthesis, secretion and action -		•	•	• 0.03
	Longevity regulating pathway - multiple species -				0.04
	Human cytomegalovirus infection -		•		0.05
	Axon guidance -		•	•	0.08
	ErbB signaling pathway-		•		0.08
	Colorectal cancer-		•		
	GABAergic synapse -		•		
	Adherens junction -			•	
	Arrhythmogenic right ventricular cardiomyopathy -			•	
	Coronavirus disease - COVID-19-			•	
	Dilated cardiomyopathy -			•	
	Aldosterone synthesis and secretion -			•	
	Rap1 signaling pathway-			•	
	cGMP-PKG signaling pathway-			•	
		- X ()	S) (6	N (4	
		SCC (10	(SF) (64	scc (66	
		NW N	М М	XSV.	
		FXF	ΧH,	Ê	
		g	ဗ်	00	
q (PM and FXS comparisons).	XEG.	KEC	Ŗ	
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OPC

KEGG

Top 20

KEGG for OPC shows enrichment for MAPK signaling (PM and FXS comparisons).

establishment of protein loca SRP-dependent cotranslation cotranslation	ization to endoplasmic reticulum - al protein targeting to membrane - al protein targeting to membrane - protein targeting to ER -				
protein loca	ization to endoplasmic reticulum -	ě	ě		
nuclear-transcribed mRNA catabolic pro	cess. nonsense-mediated decay-	- i	ě.		
	protein targeting to membrane -	ě	ě		
	viral transcription -	ĕ	ŏ		
establishment of	protein localization to membrane -	- é	ě.		
	viral gene expression -	ĕ	ĕ	_	
	translational initiation -	ě	ě.		
nuclear-tran	scribed mRNA catabolic process -	•	ě.	_	
	protein targeting -	Ó	ě.		
	mRNA catabolic process -	ě	ŏ		in a divint
	RNA catabolic process -	•	ě –	_	p.adjust
	cytoplasmic translation -	•	ě		
	detection of calcium ion -	•			0.0025
cell-cell adhesion via plasma	-membrane adhesion molecules -	•		_	0.0050
positive regulation of signal tra	nsduction by p53 class mediator-	•			0.0000
	asymmetric stem cell division -	•			0.0075
modulation o	f chemical synaptic transmission		•		
regu	lation of trans-synaptic signaling		•		
	ribosome assembly-		•		GeneRatio
rib	osomal large subunit biogenesis -		•		• 0.04
n	esponse to temperature stimulus -			•	0.04
	synapse organization				0.08
regul	ation of cellular response to heat-			•	0.12
	axonogenesis				0.16
negative regul	ation of inclusion body assembly-			•	•
	protein folding -			•	
regulation o	f neuron projection development-			•	
	cellular response to heat-			•	
	calcium-mediated signaling-			•	
	response to heat-			•	
regul	ation of inclusion body assembly-			•	
	regulation of synaptic plasticity			•	
chaperone-med	liated protein complex assembly-			•	
Cha	perone-mediated protein folding-			-	
regulation of cell morphog	enesis involved in differentiation -			•	
	'de novo' protein folding-			-	
secono	a-messenger-mediated signaling-			-	
	inclusion body assembly -			•	
		NC (65	S) (0	N (T	
		(16 C	SF) (37	U U	
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L2/3-4

GO BP

Top 20

GO for L2/3-4 shows enrichment for protein targeting (PM comparisons).



KEGG

KEGG for L2/3-4 shows enrichment for axon guidance (FXS comparisons).





positive regulation of protein polymerization	-	
adherens junction organization		
regulation of cell mornhogenesis involved in differentiation		
regulation of axonogenesis	•	
negative regulation of protein complex disassembly	•	
regulation of cellular component size	-	p.adjust 0.015
positive regulation of supramolecular fiber organization	-	0.016
regulation of protein denolymerization		0.017 0.018
	I	0.019
regulation of protein polymerization	-	
positive regulation of cytoskeleton organization	•	GeneRatio
developmental growth involved in morphogenesis	-	• 0.075
cell junction assembly		0.100
	I	0.150
protein depolymerization	-	0.175
regulation of extent of cell growth	•	
regulation of protein complex disassembly	-	
negative regulation of microtubule depolymerization	•	
positive regulation of focal adhesion assembly		
positive regulation of protein complex assembly		
regulation of cell morphogenesis	-	
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L5/6 II

Тор 20

GO BP



GO summary for cortex

Supplemental Methods: Analysis

For analysis of demographic data, one premutation case that was extremely aged is listed here as 89+ to ensure sample de-identification and sample points were removed from any graphs presented here to ensure de-identification. For premutation cluster proportion analysis, we used linear regression to determine the effect of both age and premutation status on cluster proportions. This approach is conservative, given our small sample size. We note that one young control sample had a high proportion of the committed progenitor OL I and one premutation sample demonstrated higher than expected OPC number. Additionally, the FXS case with the gene deletion demonstrated an unusually high presence of OLII.

Differential expression analysis was done with the FindMarkers functionality in Seurat (1) using settings of MAST test, padj < 0.05, and logfc.threshold = 0.25 for all cell clusters. A priori we calculated that 400 cells/condition cluster are required to detect 80% of differentially expressed genes with a false discovery rate of 5%. Thus, we are underpowered for rare cell types such as endothelial cells and Purkinje cells in which low cell numbers will make it more difficult to detect reliable changes in gene expression. We chose to omit downsampling nuclei to preserve power. Results were compared to a subset downsampled dataset for select clusters with larger nuclei number, and results were found to be similar both in the pattern of differentially regulated genes as well as the specific genes present in the data set. To ascertain the effects of age and PMI, differential expression analysis was performed using FindMarkers function in Seurat (MAST test, padj < 0.05, logfc.threshold = 0.25, latent.vars = "age" or "PMI"). We used covariate "age" and "PMI" in MAST separately. To generate a set of FMRP target genes in humans, FMRP targets that were functionally validated in human cell types were combined (2-4), and DiVenn (https://divenn.tch.harvard.edu) was used to visualize expression of this FMRP network in cellular subsets (5). Gene ontology/ enrichment analysis was conducted with clusterProfiler (6, 7) with statistical significance testing using padj (Benjamin Hochberg) < 0.05. Transcriptional regulators were identified using the RCisTarget R package (8) that utilizes the cisTarget database of gene regulators and identifies enriched transcription factor binding sites +/- 10kb for all genes. Input gene lists were taken from differential expression analysis results as described above from the premutation vs control cortical microglia and cerebellar Bergmann glia lists. A normalized enrichment score cutoff greater than 3 was used to identify significantly enriched motifs.

For pseudotime analysis, Monocle3 (9, 10) was used to recluster oligodendrocyte clusters, rescaling integrated data and regressing out the top 9 most differentially expressed genes. Spatial autocorrelation for gene expression changes across pseudotime were detected with Moran's I test (full and single branches separately). Genes were selected with q-value < 0.05 and Moran's statistic > 0.1 . To fit NB-GAM models and fitting smoothers in a condition-specific manner (tradeSeq), all genes were used for normalization but the model fitting is done only to the genes selected and the genes of interest (oligodendrocyte markers). Differential gene expression across

pseudotime between conditions (fold change greater than 2) was conducted with the Wald test, testing whether conditions are the significant variable in a model of expression along the trajectory (pseudotime). Mitochondrial genes were omitted from visualization of results given potential confounding effects.

Supplemental References

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